

SEQUENCE LISTING

<110> Ullman, Katharine
Liu, Jin
Prunuske, Amy
Dimaano, Christian

<120> METHODS AND COMPOSITIONS RELATED TO
INHIBITING NUCLEAR ENVELOPE BREAKDOWN

<130> 21101.0045U2

<150> PCT/US03/29267
<151> 2003-09-17

<150> 60/411,248
<151> 2002-09-17

<160> 35

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 5687
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 1
ttccccgctg ccagcactca ccctctctcc gctcctgctc gcaacctcgc gggttcctggg 60
gtgcttgctg ccactgtgtg gacagcgctg gcggactttt gggccggggc cgggcggcgg 120
gggaggctct ctaaggcctc cgcctctgcc tctcccgccc ccttaccgcg cccggagcgg 180
gaagcggcgg aggtccgcgc atggcctcgg gagccggagg agtcggaggg ggcgggtggcg 240
gcaagatccg gacgcggcgt tgccaccagg ggccaattaa gccttaccag caggggcgac 300
aacagcatca gggcattctt agcagggtta cagaatctgt taagaatatt gtgccagggt 360
ggctacaaag atacttcaac aagaatgaag atgtatgcag ctgttcaaca gacacaagcg 420
aggttccacg ctggccagaa aataaagagg accatctggt atatgccgat gaggagagct 480
ctaataattac tgatgggaga atcacacctg agccagcagt cagtaataca gaagaacctt 540
caacaactag tactgcttca aattatccag atgtgttaac aaggccttct cttcatcgga 600
gccatctgaa tttttccatg ttggaatccc ctgcattaca ctgtcagcca tctacatcct 660
cggcattccc aattggcagt tcgggatttt cccttgtaaa ggaaattaaa gattctacct 720
ctcagcatga tgatgataac atctcaacta ccagtggttt ttcttcaaga gcttctgata 780
aagatataac tgtttcaaag aacacttcat tgccacctct gtggtcccca gaagctgaac 840
gttctcactc actctcacag cacactgcca ccagctcaaa aaaaccagca ttcaacttgt 900
ctgccttttg aacactttcc ccttcacttg ggaattcttc aatccttaaa accagtcagc 960
ttggagattc tcctttttat cctggaaaaa caacatacgg tggggcagca gctgctgtaa 1020
gacagtctaa actacgaaat acaccttatc aggaccagt tagaagacaa atgaaagcta 1080
agcaactcag tgcacaatct tacggtgtga ccagttcaac agctcggcga atattgcagt 1140
ctttagagaa gatgtcaagc cctttagcgg atgcaaaaag aattccatcc attgtttctt 1200
ctcctctgaa ttctctctct gataggagtg gtagatgat cacagatttt caggccaaaa 1260
gagaaaagggt ggattctcaa tatcctcctg ttcacagact tatgaccca aagccagttt 1320
ccatagcaac aaatcgaagt gtttatttta aaccatctct gactccttct ggtgaattca 1380
ggaagactaa tcaaagaata gataacaagt gcagtactgg atatgaaaaa aatatgacac 1440
ccggacaaaa tagagaacaa cgagaaagtg gcttttcata tccaaatttc agtttgctg 1500
cagccaatgg tttatcttct ggagtaggtg gtggagggtg caagatgaga cgagaaagaa 1560

cacgcttttgt	tgctttctaaa	cctctggagg	aggaggaaat	ggaagttcca	gtattaccga	1620
aaatctctct	accgatcacc	agttcttcac	tgcctacctt	taatttttagt	ttccctgaga	1680
tcacaacttc	ctctccatca	cccatcaatt	cgtctcaagc	attaacaaac	aaggtagaca	1740
tgacctctcc	gagcagcact	ggcagtccca	tgtttaaatt	ttcatctcca	atcgtaaaat	1800
ctactgaggc	aaatgtacta	cctccatcat	ctattggatt	tacatttagt	gtgcctgttg	1860
caaaaacagc	agaactttct	ggttctagta	gtactttaga	accaattata	agtagttcag	1920
ctcatcatgt	cactacagtg	aacagtacaa	attgtaagaa	gacaccacct	gaagattgtg	1980
agggtccttt	tagacctgca	gaaatcctga	aagaaggaag	tgttctagat	attctgaaaa	2040
gccctgggtt	cgcacgcgcy	aagatagatt	ctggtgctgc	tcagcccacc	gcaacaagcc	2100
cagtagttta	tacaagacca	gcaataagta	gcttttcttc	tagtggaatt	gggtttgggg	2160
agagtttaaa	agctgggtca	tcatggcagt	gtgatacatg	tctactccag	aacaaagtta	2220
cagacaacaa	atgcatagcc	tgtcaagcag	caaaattgtc	acccagagat	actgctaaac	2280
agactggaat	tgaacaccca	aataaaaagt	gcaaaacaac	tctttctgca	tcaggggacag	2340
gctttggaga	caaatttaaa	ccagtgatag	gcacttggga	ttgtgatacc	tgtttagtgc	2400
aaaataaacc	tgaagcaata	aaatgtgtag	cctgtgaaac	accgaaacct	ggaacttgtg	2460
tgaagcgagc	ccttacattg	acagtgggtt	cggaaagtgc	tgagactatg	actgcttcat	2520
cttcagctg	cactgtaacc	actggtacct	taggatttgg	agataaattc	aaaaggccca	2580
ttggatcttg	ggagtgttca	gtatgctgtg	tttctaataa	tcagaagac	aataagtgtg	2640
tgctctgtat	gtctgagaaa	ccaggaagtt	cagtacctgc	ttcaagtagc	agcactgtac	2700
ctgtctctct	gtcttctgga	ggctctctag	gattggaaaa	gttcaagaaa	cccaggggaa	2760
gtggggagc	tgaattgtgc	ctagtgcaga	ataaggcaga	ctctaccaaa	tgtttggcat	2820
gtgaaagtgc	aaagccagtg	acaaaatctg	ggtttaaagg	ctttgacaca	tcttctcat	2880
cttcgaactc	agcagcctcc	tcctccttca	aatttgggtg	ctcatcatcc	tcttctgggc	2940
cttctcagac	tttaacaagc	actggaaatt	ttaaatttgg	agatcaggga	ggattcaaaa	3000
taggtgtgtc	atctgattct	gggtctataa	accccatgag	tgaaggcttt	aaattttcta	3060
aaccaatagg	agattttaaa	tttgaggttt	catctgaatc	taagcccga	gaagttaaaa	3120
aagatagtaa	gaatgataat	tttaagtttg	gactttcttc	tggtttaagc	aaccagttt	3180
ctttaactcc	atttcaattt	gggttatcta	atcttggaca	ggaagaaaag	aaagagggaac	3240
tgcceaaatc	ttcctctgca	ggtttttagt	ttggtagagg	tgttattaac	tccacccttg	3300
ctcctgctaa	cacctagtgc	acctctgaga	acaagagcag	cttcaacctt	ggaaccatag	3360
aaaccaagag	tgcttcagtg	gctcctttca	catgtaagac	atcagaagct	aaaaaagaag	3420
aaatgctgc	caccaaaagg	ggattctctt	ttggcaacgt	ggagcctgcc	tctctgccat	3480
ctgcctcagt	gtttgttttg	ggaaggacag	aagagaaaca	gcaagagcct	gtcacttcta	3540
cttccttagt	ttttgggaag	aaagctgaca	atgaagagcc	aaagtgtcaa	ccagtgtttt	3600
cctttgggaa	ttcagagcaa	accaaagatg	agaattcttc	aaagtccaca	tttagtttta	3660
gtatgacaaa	accatctgag	aaggaatctg	aacagccagc	aaaagccact	tttgcctttg	3720
gagctcaaac	tagtactaca	gctgatcaag	gtgcagcaaa	gccagttttt	agtttcttga	3780
acaacagttc	ctctagtcca	agtacaccag	ccacttctgc	tggtgggtggc	atatttggtta	3840
gttccacctc	ttcctccaat	ccacctgtgg	ctacctttgt	gtttggacag	tccagcaatc	3900
ctgtgagcag	ctctgccttt	ggtaacactg	ctgaatccag	cacctctcag	tctttgctat	3960
tttctcaaga	tagcaaaacta	gcaaccacat	ccagcacagg	tacagctgtc	accccatattg	4020
tctttgggtcc	aggagccagc	agtaataata	ctaccacctc	tggtttcggc	tttggagcca	4080
caaccacatc	tagctctgca	ggatcctcct	ttgtatttgg	aactggacct	tcagcaccat	4140
ctgccagtc	agcattttgt	gctaaccaga	ccccaacatt	tggacaaagt	caaggtgcca	4200
gccagcccaa	tccccaggc	tttgatctta	tatcatcttc	cacagcattha	tttcccactg	4260
gttctcagcc	tgcaccacct	acttttggga	cagtgtcaag	cagtagccag	ccccctgtgt	4320
ttggacagca	acctagtgcg	tctgcatttg	gctctggaac	aactcctaata	tctagttcgg	4380
ctttccagtt	tggcagcagc	actacaaatt	tcaacttcac	aaacaacagt	ccatcaggag	4440
tgttcacatt	tgggtgcaaat	tctagcacac	ctgcagcctc	agcccagcct	tcaggctcgg	4500
ggggctttcc	atttaaccag	tctccagcag	cattttacagt	ggggtcaaat	gggaaaaatg	4560
tgttctcttc	ttctggaact	tcattctctg	gtcgcaagat	aaagactgct	gttagacgca	4620
ggaaataaag	gtcacattgg	tgttgtactc	aatttttaaca	acagctgggtg	ccctgctttc	4680
agatactgga	ttgtactttg	tgctggggtt	atctgaagtc	agatctgcct	aaggacttct	4740
ttaatttttg	aattttcttc	ctttctcttt	cgttacagaa	gccccaccct	gcctcaccca	4800
ccttttttta	aataaataaa	tagctagact	ggtgactgat	tcttcagcaa	aaatatttta	4860
gtaccagca	gattattcac	tgatttgaca	tagtctggct	gtaccagga	atggagcctg	4920
cacggtgaat	ggctttgtat	agaacctctt	tgtctacacc	attatgtgcg	ctgataagcg	4980
ttcatggaac	gcgttgaaat	tgtaattata	tctgaggaat	tctgtataga	ttagaattct	5040
gtatagatta	gagagtgttg	aaacggatga	tttctatgct	gagtttgtgc	tggtgtatgt	5100
gtgaagtgcg	tgagttgggt	gtattgtgcg	ctaaactttt	ctgatagagg	aagcctgatt	5160
aaagaatggt	ccgtgctaag	gacttggttag	atctagttca	ctctccattt	aataattata	5220

```

tgctatttct atattttcat tctcctatca cctgtcttgc ctttttcatt attttattat 5280
gaaacttggtg taaatacaat tttgtttctg tactttttgg cataacataa atctgtgaac 5340
ttgaaatttg aatttttgtg tagagatttt tttgttggtt gtttagtctt gtctcagatt 5400
ttattatgta aatccccatta ttcaaagttg cctaaatcca tttggaaatc tttaaaaaaa 5460
aaattgggga ttcttaaagt tgaattttatt ggctttttctg atccagtttt gtttggacca 5520
aaaaccagta ttgtacaaag tattaagcat atatttttat atttactaaa atggactgtg 5580
gtgacttttg ataataagga aaagtttaat attaaagcca tgttttattac agtataatta 5640
acatgttaaa ccatgggata aatgccatca ataaaaaatt atgacat 5687

```

<210> 2

<211> 1475

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 2

```

Met Ala Ser Gly Ala Gly Gly Val Gly Gly Gly Gly Gly Gly Lys Ile
 1           5           10           15
Arg Thr Arg Arg Cys His Gln Gly Pro Ile Lys Pro Tyr Gln Gln Gly
 20           25           30
Arg Gln Gln His Gln Gly Ile Leu Ser Arg Val Thr Glu Ser Val Lys
 35           40           45
Asn Ile Val Pro Gly Trp Leu Gln Arg Tyr Phe Asn Lys Asn Glu Asp
 50           55           60
Val Cys Ser Cys Ser Thr Asp Thr Ser Glu Val Pro Arg Trp Pro Glu
 65           70           75           80
Asn Lys Glu Asp His Leu Val Tyr Ala Asp Glu Glu Ser Ser Asn Ile
 85           90           95
Thr Asp Gly Arg Ile Thr Pro Glu Pro Ala Val Ser Asn Thr Glu Glu
100           105           110
Pro Ser Thr Thr Ser Thr Ala Ser Asn Tyr Pro Asp Val Leu Thr Arg
115           120           125
Pro Ser Leu His Arg Ser His Leu Asn Phe Ser Met Leu Glu Ser Pro
130           135           140
Ala Leu His Cys Gln Pro Ser Thr Ser Ser Ala Phe Pro Ile Gly Ser
145           150           155           160
Ser Gly Phe Ser Leu Val Lys Glu Ile Lys Asp Ser Thr Ser Gln His
165           170           175
Asp Asp Asp Asn Ile Ser Thr Thr Ser Gly Phe Ser Ser Arg Ala Ser
180           185           190
Asp Lys Asp Ile Thr Val Ser Lys Asn Thr Ser Leu Pro Pro Leu Trp
195           200           205
Ser Pro Glu Ala Glu Arg Ser His Ser Leu Ser Gln His Thr Ala Thr
210           215           220
Ser Ser Lys Lys Pro Ala Phe Asn Leu Ser Ala Phe Gly Thr Leu Ser
225           230           235           240
Pro Ser Leu Gly Asn Ser Ser Ile Leu Lys Thr Ser Gln Leu Gly Asp
245           250           255
Ser Pro Phe Tyr Pro Gly Lys Thr Thr Tyr Gly Gly Ala Ala Ala
260           265           270
Val Arg Gln Ser Lys Leu Arg Asn Thr Pro Tyr Gln Ala Pro Val Arg
275           280           285
Arg Gln Met Lys Ala Lys Gln Leu Ser Ala Gln Ser Tyr Gly Val Thr
290           295           300
Ser Ser Thr Ala Arg Arg Ile Leu Gln Ser Leu Glu Lys Met Ser Ser
305           310           315           320

```

Pro Leu Ala Asp Ala Lys Arg Ile Pro Ser Ile Val Ser Ser Pro Leu
 325 330 335
 Asn Ser Pro Leu Asp Arg Ser Gly Ile Asp Ile Thr Asp Phe Gln Ala
 340 345 350
 Lys Arg Glu Lys Val Asp Ser Gln Tyr Pro Pro Val Gln Arg Leu Met
 355 360 365
 Thr Pro Lys Pro Val Ser Ile Ala Thr Asn Arg Ser Val Tyr Phe Lys
 370 375 380
 Pro Ser Leu Thr Pro Ser Gly Glu Phe Arg Lys Thr Asn Gln Arg Ile
 385 390 395 400
 Asp Asn Lys Cys Ser Thr Gly Tyr Glu Lys Asn Met Thr Pro Gly Gln
 405 410 415
 Asn Arg Glu Gln Arg Glu Ser Gly Phe Ser Tyr Pro Asn Phe Ser Leu
 420 425 430
 Pro Ala Ala Asn Gly Leu Ser Ser Gly Val Gly Gly Gly Gly Lys
 435 440 445
 Met Arg Arg Glu Arg Thr Arg Phe Val Ala Ser Lys Pro Leu Glu Glu
 450 455 460
 Glu Glu Met Glu Val Pro Val Leu Pro Lys Ile Ser Leu Pro Ile Thr
 465 470 475 480
 Ser Ser Ser Leu Pro Thr Phe Asn Phe Ser Ser Pro Glu Ile Thr Thr
 485 490 495
 Ser Ser Pro Ser Pro Ile Asn Ser Ser Gln Ala Leu Thr Asn Lys Val
 500 505 510
 Gln Met Thr Ser Pro Ser Ser Thr Gly Ser Pro Met Phe Lys Phe Ser
 515 520 525
 Ser Pro Ile Val Lys Ser Thr Glu Ala Asn Val Leu Pro Pro Ser Ser
 530 535 540
 Ile Gly Phe Thr Phe Ser Val Pro Val Ala Lys Thr Ala Glu Leu Ser
 545 550 555 560
 Gly Ser Ser Ser Thr Leu Glu Pro Ile Ile Ser Ser Ser Ala His His
 565 570 575
 Val Thr Thr Val Asn Ser Thr Asn Cys Lys Lys Thr Pro Pro Glu Asp
 580 585 590
 Cys Glu Gly Pro Phe Arg Pro Ala Glu Ile Leu Lys Glu Gly Ser Val
 595 600 605
 Leu Asp Ile Leu Lys Ser Pro Gly Phe Ala Ser Pro Lys Ile Asp Ser
 610 615 620
 Val Ala Ala Gln Pro Thr Ala Thr Ser Pro Val Val Tyr Thr Arg Pro
 625 630 635 640
 Ala Ile Ser Ser Phe Ser Ser Ser Gly Ile Gly Phe Gly Glu Ser Leu
 645 650 655
 Lys Ala Gly Ser Ser Trp Gln Cys Asp Thr Cys Leu Leu Gln Asn Lys
 660 665 670
 Val Thr Asp Asn Lys Cys Ile Ala Cys Gln Ala Ala Lys Leu Ser Pro
 675 680 685
 Arg Asp Thr Ala Lys Gln Thr Gly Ile Glu Thr Pro Asn Lys Ser Gly
 690 695 700
 Lys Thr Thr Leu Ser Ala Ser Gly Thr Gly Phe Gly Asp Lys Phe Lys
 705 710 715 720
 Pro Val Ile Gly Thr Trp Asp Cys Asp Thr Cys Leu Val Gln Asn Lys
 725 730 735
 Pro Glu Ala Ile Lys Cys Val Ala Cys Glu Thr Pro Lys Pro Gly Thr
 740 745 750
 Cys Val Lys Arg Ala Leu Thr Leu Thr Val Val Ser Glu Ser Ala Glu
 755 760 765
 Thr Met Thr Ala Ser Ser Ser Ser Cys Thr Val Thr Thr Gly Thr Leu
 770 775 780
 Gly Phe Gly Asp Lys Phe Lys Arg Pro Ile Gly Ser Trp Glu Cys Ser
 785 790 795 800

Val	Cys	Cys	Val	Ser	Asn	Asn	Ala	Glu	Asp	Asn	Lys	Cys	Val	Ser	Cys		
				805					810						815		
Met	Ser	Glu	Lys	Pro	Gly	Ser	Ser	Val	Pro	Ala	Ser	Ser	Ser	Ser	Ser	Thr	
			820					825						830			
Val	Pro	Val	Ser	Leu	Pro	Ser	Gly	Gly	Ser	Leu	Gly	Leu	Glu	Lys	Phe		
			835				840						845				
Lys	Lys	Pro	Glu	Gly	Ser	Trp	Asp	Cys	Glu	Leu	Cys	Leu	Val	Gln	Asn		
			850			855					860						
Lys	Ala	Asp	Ser	Thr	Lys	Cys	Leu	Ala	Cys	Glu	Ser	Ala	Lys	Pro	Gly		
865					870					875					880		
Thr	Lys	Ser	Gly	Phe	Lys	Gly	Phe	Asp	Thr	Ser	Ser	Ser	Ser	Ser	Asn		
				885					890						895		
Ser	Ala	Ala	Ser	Ser	Ser	Phe	Lys	Phe	Gly	Val	Ser	Ser	Ser	Ser	Ser		
			900					905						910			
Gly	Pro	Ser	Gln	Thr	Leu	Thr	Ser	Thr	Gly	Asn	Phe	Lys	Phe	Gly	Asp		
			915				920						925				
Gln	Gly	Gly	Phe	Lys	Ile	Gly	Val	Ser	Ser	Asp	Ser	Gly	Ser	Ile	Asn		
			930			935						940					
Pro	Met	Ser	Glu	Gly	Phe	Lys	Phe	Ser	Lys	Pro	Ile	Gly	Asp	Phe	Lys		
945					950					955					960		
Phe	Gly	Val	Ser	Ser	Glu	Ser	Lys	Pro	Glu	Glu	Val	Lys	Lys	Asp	Ser		
				965					970					975			
Lys	Asn	Asp	Asn	Phe	Lys	Phe	Gly	Leu	Ser	Ser	Gly	Leu	Ser	Asn	Pro		
			980				985							990			
Val	Ser	Leu	Thr	Pro	Phe	Gln	Phe	Gly	Val	Ser	Asn	Leu	Gly	Gln	Glu		
			995				1000						1005				
Glu	Lys	Lys	Glu	Glu	Leu	Pro	Lys	Ser	Ser	Ser	Ala	Gly	Phe	Ser	Phe		
			1010			1015					1020						
Gly	Thr	Gly	Val	Ile	Asn	Ser	Thr	Pro	Ala	Pro	Ala	Asn	Thr	Ile	Val		
1025					1030					1035					1040		
Thr	Ser	Glu	Asn	Lys	Ser	Ser	Phe	Asn	Leu	Gly	Thr	Ile	Glu	Thr	Lys		
				1045					1050					1055			
Ser	Ala	Ser	Val	Ala	Pro	Phe	Thr	Cys	Lys	Thr	Ser	Glu	Ala	Lys	Lys		
			1060					1065					1070				
Glu	Glu	Met	Pro	Ala	Thr	Lys	Gly	Gly	Phe	Ser	Phe	Gly	Asn	Val	Glu		
		1075				1080					1085						
Pro	Ala	Ser	Leu	Pro	Ser	Ala	Ser	Val	Phe	Val	Leu	Gly	Arg	Thr	Glu		
		1090				1095					1100						
Glu	Lys	Gln	Gln	Glu	Pro	Val	Thr	Ser	Thr	Ser	Leu	Val	Phe	Gly	Lys		
1105					1110					1115					1120		
Lys	Ala	Asp	Asn	Glu	Glu	Pro	Lys	Cys	Gln	Pro	Val	Phe	Ser	Phe	Gly		
				1125					1130					1135			
Asn	Ser	Glu	Gln	Thr	Lys	Asp	Glu	Asn	Ser	Ser	Lys	Ser	Thr	Phe	Ser		
			1140					1145					1150				
Phe	Ser	Met	Thr	Lys	Pro	Ser	Glu	Lys	Glu	Ser	Glu	Gln	Pro	Ala	Lys		
		1155				1160						1165					
Ala	Thr	Phe	Ala	Phe	Gly	Ala	Gln	Thr	Ser	Thr	Thr	Ala	Asp	Gln	Gly		
			1170			1175					1180						
Ala	Ala	Lys	Pro	Val	Phe	Ser	Phe	Leu	Asn	Asn	Ser	Ser	Ser	Ser	Ser		
1185					1190					1195					1200		
Ser	Thr	Pro	Ala	Thr	Ser	Ala	Gly	Gly	Gly	Ile	Phe	Gly	Ser	Ser	Thr		
				1205					1210					1215			
Ser	Ser	Ser	Asn	Pro	Pro	Val	Ala	Thr	Phe	Val	Phe	Gly	Gln	Ser	Ser		
			1220					1225					1230				
Asn	Pro	Val	Ser	Ser	Ser	Ala	Phe	Gly	Asn	Thr	Ala	Glu	Ser	Ser	Thr		
		1235				1240						1245					
Ser	Gln	Ser	Leu	Leu	Phe	Ser	Gln	Asp	Ser	Lys	Leu	Ala	Thr	Thr	Ser		
		1250				1255					1260						
Ser	Thr	Gly	Thr	Ala	Val	Thr	Pro	Phe	Val	Phe	Gly	Pro	Gly	Ala	Ser		
1265					1270					1275					1280		

Ser Asn Asn Thr Thr Thr Ser Gly Phe Gly Phe Gly Ala Thr Thr Thr
 1285 1290 1295
 Ser Ser Ser Ala Gly Ser Ser Phe Val Phe Gly Thr Gly Pro Ser Ala
 1300 1305 1310
 Pro Ser Ala Ser Pro Ala Phe Gly Ala Asn Gln Thr Pro Thr Phe Gly
 1315 1320 1325
 Gln Ser Gln Gly Ala Ser Gln Pro Asn Pro Pro Gly Phe Gly Ser Ile
 1330 1335 1340
 Ser Ser Ser Thr Ala Leu Phe Pro Thr Gly Ser Gln Pro Ala Pro Pro
 1345 1350 1355 1360
 Thr Phe Gly Thr Val Ser Ser Ser Ser Gln Pro Pro Val Phe Gly Gln
 1365 1370 1375
 Gln Pro Ser Gln Ser Ala Phe Gly Ser Gly Thr Thr Pro Asn Ser Ser
 1380 1385 1390
 Ser Ala Phe Gln Phe Gly Ser Ser Thr Thr Asn Phe Asn Phe Thr Asn
 1395 1400 1405
 Asn Ser Pro Ser Gly Val Phe Thr Phe Gly Ala Asn Ser Ser Thr Pro
 1410 1415 1420
 Ala Ala Ser Ala Gln Pro Ser Gly Ser Gly Gly Phe Pro Phe Asn Gln
 1425 1430 1435 1440
 Ser Pro Ala Ala Phe Thr Val Gly Ser Asn Gly Lys Asn Val Phe Ser
 1445 1450 1455
 Ser Ser Gly Thr Ser Phe Ser Gly Arg Lys Ile Lys Thr Ala Val Arg
 1460 1465 1470
 Arg Arg Lys
 1475

<210> 3

<211> 1200

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 3

atggcggcag	ccggaggagg	aggccctggt	ggtccaggaa	ccggggggcaa	aatacgcagt	60
aggagatatc	acttgagttc	cggcaggact	ccgtacagca	agagccggca	gcggcagcag	120
ggatcatca	gccgtgtcac	ggatactgtc	aagagcattg	ttcctggatg	gttgcaagaag	180
tattttaaca	aacaagaaga	ggaacatgac	cgagtacata	gtgcaagtga	agtaattgtg	240
aatgatactg	aggctagaga	aaataatgct	caacaccata	tatatgatga	tgatgatgaa	300
gaaggaaatt	ctcccactga	tggcagagtc	actcctgagc	cagttattaa	tgttgatgaa	360
gaagttccgt	ccactagtca	gtcagcaata	aacaacacag	atgcccttac	taggccatct	420
ttacaccgtg	ctagtctaaa	cttcaacata	tttgactctc	ctgcactgaa	ctgccagcct	480
tcaacctctt	cggcatttcc	tattggcacc	tctggcttct	cacttataaa	agagatcaag	540
gactctacct	cgcaacatga	tgacgataac	atctccacca	ccagtggctt	tacctctaga	600
gcatctgata	aggatctagc	cgtttcaaaa	aatgtcagcg	tgccacctct	ttggtctcct	660
gaagttgata	gctcacagtc	tctgtcacat	aactcctcca	tgacctccaa	aaaaccaact	720
tttaatcttt	ctgctttcgg	ttctctctca	ccttctcttg	gaaacgcata	tatcttaaac	780
cgtcagcttg	gtgattctcc	tttttatcct	ggcaaaacaa	cataccaagg	tgcaactgca	840
gtccgttcct	cgcgagtgcg	cgccacccca	tatcaagcac	ctttacgaag	acaggtgaag	900
gcaaaaccag	cagcacactc	tcagcagtg	ggtgttacca	gctccgctgc	acgccgcatt	960
ctacagtctt	tggagaagat	gtcaagtcct	ttagcggatg	ccaaaaggat	cccatacaac	1020
tcttctttat	cacatacacc	agaaaagaac	gtcatggata	ttcccgaaaa	cccatacaaa	1080
aggaaaaagg	tggagtcccc	atttcctcca	gttcagaggc	tcgtgactcc	aaaatccatt	1140
tctgtctctg	caaaccgttc	cctgtatatc	aagccttcac	tgacaccatc	tgctgtatca	1200

<210> 4

<211> 400

<212> PRT

<223> Description of Artificial Sequence:/note =
synthetic construct

Met 1	Ala	Ala	Ala	Gly 5	Gly	Gly	Gly	Pro	Gly 10	Gly	Pro	Gly	Thr	Gly 15	Gly
Lys	Ile	Arg	Ser	Arg	Arg	Tyr	His	Leu	Ser	Ser	Gly	Arg	Thr	Pro	Tyr
			20					25					30		
Ser	Lys	Ser	Arg	Gln	Arg	Gln	Gln	Gly	Ile	Ile	Ser	Arg	Val	Thr	Asp
		35				40					45				
Thr	Val	Lys	Ser	Ile	Val	Pro	Gly	Trp	Leu	Gln	Lys	Tyr	Phe	Asn	Lys
	50					55					60				
Gln	Glu	Glu	Glu	His	Asp	Arg	Val	His	Ser	Ala	Ser	Glu	Val	Ile	Val
65					70					75					80
Asn	Asp	Thr	Glu	Ala	Arg	Glu	Asn	Asn	Ala	Gln	His	His	Ile	Tyr	Asp
				85					90					95	
Asp	Asp	Asp	Glu	Glu	Gly	Asn	Ser	Pro	Thr	Asp	Gly	Arg	Val	Thr	Pro
		100				105							110		
Glu	Pro	Val	Ile	Asn	Val	Asp	Glu	Glu	Val	Pro	Ser	Thr	Ser	Gln	Ser
		115				120						125			
Ala	Ile	Asn	Asn	Thr	Asp	Ala	Leu	Thr	Arg	Pro	Ser	Leu	His	Arg	Ala
	130					135					140				
Ser	Leu	Asn	Phe	Asn	Ile	Phe	Asp	Ser	Pro	Ala	Leu	Asn	Cys	Gln	Pro
145					150					155					160
Ser	Thr	Ser	Ser	Ala	Phe	Pro	Ile	Gly	Thr	Ser	Gly	Phe	Ser	Leu	Ile
				165					170					175	
Lys	Glu	Ile	Lys	Asp	Ser	Thr	Ser	Gln	His	Asp	Asp	Asp	Asn	Ile	Ser
			180					185					190		
Thr	Thr	Ser	Gly	Phe	Thr	Ser	Arg	Ala	Ser	Asp	Lys	Asp	Leu	Ala	Val
		195					200					205			
Ser	Lys	Asn	Val	Ser	Val	Pro	Pro	Leu	Trp	Ser	Pro	Glu	Val	Asp	Arg
	210					215					220				
Ser	Gln	Ser	Leu	Ser	His	Asn	Ser	Ser	Met	Thr	Ser	Lys	Lys	Pro	Thr
225					230					235					240
Phe	Asn	Leu	Ser	Ala	Phe	Gly	Ser	Leu	Ser	Pro	Ser	Leu	Gly	Asn	Ala
				245					250					255	
Ser	Ile	Leu	Asn	Arg	Gln	Leu	Gly	Asp	Ser	Pro	Phe	Tyr	Pro	Gly	Lys
			260					265					270		
Thr	Thr	Tyr	Gln	Gly	Ala	Ala	Ala	Val	Arg	Ser	Ser	Arg	Val	Arg	Ala
		275					280					285			
Thr	Pro	Tyr	Gln	Ala	Pro	Leu	Arg	Arg	Gln	Val	Lys	Ala	Lys	Pro	Ala
	290					295					300				
Ala	His	Ser	Gln	Gln	Cys	Gly	Val	Thr	Ser	Ser	Ala	Ala	Arg	Arg	Ile
305					310					315					320
Leu	Gln	Ser	Leu	Glu	Lys	Met	Ser	Ser	Pro	Leu	Ala	Asp	Ala	Lys	Arg
				325					330					335	
Ile	Pro	Ser	Asn	Ser	Ser	Leu	Ser	His	Thr	Pro	Glu	Lys	Asn	Val	Met
			340					345					350		
Asp	Ile	Pro	Glu	Asn	Pro	Ser	Lys	Arg	Lys	Lys	Val	Glu	Ser	Pro	Phe

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 5

cgcaaaccgt	tccctgtata	tcaagccttc	actgacacca	tctgctgtat	caaatacaaaa	60
cagtcgcaga	atacagccag	acaagcacaa	tgagtccaca	aagaataatc	tgcaatcaac	120
atctcagttc	cacagcttct	cttaccctaaa	gttcagtact	ccggcatcca	atggattgtc	180
atcaggaaca	ggtggtggca	aaatgatgag	ggaaaaaggc	tctcattact	caacaaagcc	240
agctaattgag	gagctggatg	ggcctgtttt	acctgaaatc	ccattgcctc	ttagcacagc	300
agcccttccc	agctttcaat	tttcaacttt	gtctggctct	gctacttcgc	ctatctctgt	360
cactaaacct	gcaaacagta	cgacatgtca	cttaaccagc	agtagtccat	cgttcacatt	420
ttcgtccctt	attgtaaaat	cgactgaatc	aaatgctcag	ttttctggct	catctgttga	480
tttcactttc	agtgtaccag	cagcgaaagc	gtcatctgca	acatctgatg	agagcaaggt	540
gtctgctgta	agtagcgcg	ctaaaacaca	tgctgctggt	aatagcagtg	caaagaacac	600
tgatgatgaa	caagtgggat	tctgtaaacc	tgcaaaaact	ctgaaggaag	ggagtgtgtt	660
agacatgctg	agaagtccag	ggttttcttc	tttaccctcc	ctgctaactt	cagaatcaac	720
tcttaacaga	agcacaccaa	ccctctcaaa	gactgtgggg	aatacattct	cccctgcaaa	780
tgtatcatta	ggagttagga	gcaagcaatt	tggactttgg	caatgcagcg	catgctttca	840
tgagaatatg	tcatctgata	gcaactgtat	ttcttgctct	gctgtaaaac	ctcggcctac	900
agaaacctct	aagaaactac	ctgcttcacc	accaagtagc	aatacaaaaa	gcactgtccc	960
actttctagc	acaccaggac	taggagacat	atttaaaaaa	cctgcaggca	tgtgggattg	1020
tgacacttgt	ttagtacaga	acaaagcaga	agtaacaaaa	tgtgttgctt	gtgaaacccc	1080
caaacctggg	acttgtataa	aagctacctt	gttgataccg	tccaccacaa	agtctataaa	1140
tccagccaca	aatacccttg	cttttgcctc	ttgctctgca	agcattccaa	atgaagaaat	1200
gttcaaaaag	cctatgggat	cttgggagtg	cacagtttgt	catatgcaga	ataaaacaga	1260
ggataataca	tgtgtgggct	gcaaagctga	gaaaccagga	accgtcaaga	gcgtacctac	1320
tgctgcacca	tcagggctgc	tgggatttgt	acatcagttt	aaaaaaccaa	cagggagctg	1380
ggatttgtat	gtctgcttaa	tacaaaacaa	accagaagcc	gccaaatgta	ttgcatgtga	1440
aagtgccaaa	ccaggcacca	aagcagaacc	gaaaggtagt	tttgatacag	tgaaaaattc	1500
cgtttcagtt	gcaccccttt	cttcagggca	gctgggattg	ttagatcagt	ttaagaagtc	1560
ggcaggaagc	tgggatttgt	atgtctgcct	agtagaaaac	aaaccagaag	ccacaaaatg	1620
tgttgcctgt	gagacctcaa	aaccaggcac	aaaagcagaa	ttaaaagggt	ttggaacatc	1680
aaccttttcc	tctggaacag	cagctccgac	cttcaagttt	gggtgtgcag	cttcagatag	1740
cactgctgag	ttaaaatcgg	gtgcctctac	aagtggtttt	gccaaatcta	taggggattt	1800
taaattttgt	ttagtgtctg	catccacaa	aacagaggaa	actggcaaga	aaagctttac	1860
atttggctct	tctactacca	atgaagtttc	agcaggtttt	aagtttggca	ttgcccgttc	1920
tgctcagaca	aaaccagaca	ccctaagtca	gtctaccaca	agtggtttca	catttggttc	1980
tgttttccaa	acggttttct	ttgctcctgc	tgcaactagc	tcacgcagta	caggcttgca	2040
agtggcggtc	gcaattgctg	attccaacct	tgcaactact	gctgccttga	aatcagcaga	2100
agagaaaaag	gcccgaagcac	ctacaataac	accgttttct	tttgggaaaa	cagatcaaaa	2160
taaagagact	gcattccacct	cttttgtctt	tggaaagaaa	gatgaaaaga	cagactctgc	2220
tccaactgga	tcttcccttg	cttttgggct	aaaaaaggat	ggggaggaat	ctaagccgtt	2280
tcttttttga	aaacctgagc	caaccaaagt	agatggcaat	gcagcatctg	ctggttttgc	2340
ttttggtgtg	actaatccca	cagagaaaaa	ggatattgaa	cagcctggaa	aatcagtttt	2400
tgcttccggt	gctcaaaact	caatcacaga	tgctggagct	tccaagcaac	cttttagttt	2460
tctgaccaat	gtctcctcca	ctgcagcttc	atcaagcaat	tgtgggtgtt	ccagcagtg	2520
atltggcagt	gtgactcagt	caagcactcc	tgcaaccctc	agtaatgtgt	ttggcagtc	2580
tatttcagca	aatgctcctg	ccccgtctag	tgggtgattt	ggaaacctca	ctccatcaaa	2640
tgcccttgca	gcttctagca	ctttgtttgg	taacgttget	ccctcaagta	ctccttctgg	2700
ctccagtggt	ttgtttggca	ctgcagctgc	atccagtagt	cctgccactt	ccactagctt	2760
gtttggctct	gcagctaaat	cgagtgtctc	tgcaagctct	ggaggggtgt	tcaacagtc	2820
agctcctgct	gccccagcat	caactacaat	tagtgtgttt	ggcagtgtag	cctcttcaac	2880
aaacattctt	gcaaatcttg	caaacataat	tggagctctc	ggtggagcgg	ccactgctcc	2940
tggggctttt	gtgtttggac	agccagctag	tactgctagc	actgtttttg	gaaactcgag	3000
cgaatcaaaa	tcgacctttg	ttttctctgg	tcaggaaaaa	aaacctcgta	cctctgcaag	3060
tacctctgtg	actccatttc	tatttggagc	agtgtctgcc	actactacce	cagcagctcc	3120
aagttttaac	tttggacgaa	caatcacttc	aaatacaaca	ggcactagct	cgtctccatt	3180
tatctttggt	gctgggtgcaa	gtggctctgc	ttcttcaagt	ataacggctc	aggccaatcc	3240


```

agtgccagca tttgggcaaa gttctaatacc gtctactgca cccgcttttg gctcttcaac 3300
ttcagttcca gtgtttccag ctgggagttc tcagcaagtc ccggcctttg gttcgagtag 3360
tgcacaaccc cctgtgtttg ggcaacaagc cgctcagcct tcttttgat ctctgtctgc 3420
accagtgct ggatctggtt tcccgtttgg caacaacgca aacttcaact ttaacagcac 3480
aaattcatca ggtggagtct tcacgtttta tgcaaattca ggatccacca cccaaccacc 3540
tccccagga tacatgttta atgcagctgc gccaggtttt aacataggaa cgaatggcag 3600
gactactcca gcatctacta tttctactcg caagataaag accgccagaa gaagaaagta 3660
attgaatgaa tgtactggaa gtaatggttg tttcaagaaa tgaatggtgt ccctgcattg 3720
tgcaaatact ggagtgttcc tcatgctgtg tgtagtggaa gtcagatcag cccaaggaca 3780
aaaatatatg ctgaaacttg tctctttttc ctctgtaatt aaaacatggg gatgggaaat 3840
ttcttaacca agaaatctga ttccggcgcc tcctttgttt acctgacttg gcatgatttg 3900
gctatacgag tgtttatagc ctgcacagcg aatggctttt gtataatacc tctttcatct 3960
gcaccactat tttattgatg ctttgaaatt gtaattgtga gtgaggagcc gtgtataggt 4020
tacagactga tttctacacc acagtgtgtc tgggtgaatgt gtggagcgga gtgtagtgtg 4080
caccgaaact tttctgctta cggaagactg actcatgaat ggtccttaca taggatgtgc 4140
tagatctgta cttctctttc aaatatatgc cttttcttct ccttctctct cccctgttt 4200
tcattcagct cttgtcatct tctccattat tttattatat tcatgtaa atacatttgttt 4260
ctccatgtac ctttcagcat aaactaaatc aaaaaaaaaa aaaaa 4305

```

<210> 6

<211> 1219

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 6

```

Ala Asn Arg Ser Leu Tyr Ile Lys Pro Ser Leu Thr Pro Ser Ala Val
 1              5              10              15
Ser Asn Thr Asn Ser Arg Arg Ile Gln Pro Asp Lys His Asn Glu Ser
      20              25              30
Thr Lys Asn Asn Leu Gln Ser Thr Ser Gln Ser His Ser Phe Ser Tyr
      35              40              45
Pro Lys Phe Ser Thr Pro Ala Ser Asn Gly Leu Ser Ser Gly Thr Gly
      50              55              60
Gly Gly Lys Met Met Arg Glu Lys Gly Ser His Tyr Ser Thr Lys Pro
65              70              75              80
Ala Asn Glu Glu Leu Asp Gly Pro Val Leu Pro Glu Ile Pro Leu Pro
      85              90              95
Leu Ser Thr Ala Ala Leu Pro Ser Phe Gln Phe Ser Thr Leu Ser Gly
      100             105             110
Ser Ala Thr Ser Pro Ile Ser Val Thr Lys Pro Ala Asn Ser Thr Thr
      115             120             125
Cys His Leu Thr Ser Ser Ser Pro Ser Phe Thr Phe Ser Ser Pro Ile
      130             135             140
Val Lys Ser Thr Glu Ser Asn Ala Gln Phe Ser Gly Ser Ser Val Asp
145             150             155             160
Phe Thr Phe Ser Val Pro Ala Ala Lys Ala Ser Ser Ala Thr Ser Asp
      165             170             175
Glu Ser Lys Val Ser Ala Val Ser Ser Ala Ala Lys Thr His Ala Ala
      180             185             190
Val Asn Ser Ser Ala Lys Asn Thr Asp Asp Glu Gln Val Gly Phe Cys
      195             200             205
Lys Pro Ala Lys Thr Leu Lys Glu Gly Ser Val Leu Asp Met Leu Arg
      210             215             220
Ser Pro Gly Phe Ser Ser Leu Pro Ser Leu Leu Thr Ser Glu Ser Thr
225             230             235             240
Leu Asn Arg Ser Thr Pro Thr Leu Ser Lys Thr Val Gly Asn Thr Phe
      245             250             255

```

Ser	Pro	Ala	Asn	Val	Ser	Leu	Gly	Val	Gly	Ser	Lys	Gln	Phe	Gly	Leu		
			260					265					270				
Trp	Gln	Cys	Ser	Ala	Cys	Phe	His	Glu	Asn	Met	Ser	Ser	Asp	Ser	Asn		
		275					280					285					
Cys	Ile	Ser	Cys	Ser	Ala	Val	Lys	Pro	Arg	Pro	Thr	Glu	Thr	Ser	Lys		
	290					295					300						
Lys	Leu	Pro	Ala	Ser	Pro	Pro	Ser	Ser	Asn	Thr	Lys	Ser	Thr	Val	Pro		
305					310					315					320		
Leu	Ser	Ser	Thr	Pro	Gly	Leu	Gly	Asp	Ile	Phe	Lys	Lys	Pro	Ala	Gly		
				325					330					335			
Met	Trp	Asp	Cys	Asp	Thr	Cys	Leu	Val	Gln	Asn	Lys	Ala	Glu	Val	Thr		
			340					345					350				
Lys	Cys	Val	Ala	Cys	Glu	Thr	Pro	Lys	Pro	Gly	Thr	Cys	Ile	Lys	Ala		
		355					360					365					
Thr	Leu	Leu	Ile	Pro	Ser	Thr	Thr	Lys	Ser	Ile	Asn	Pro	Ala	Thr	Asn		
	370					375					380						
Thr	Leu	Ala	Phe	Ala	Ser	Cys	Ser	Ala	Ser	Ile	Pro	Asn	Glu	Glu	Met		
385					390					395					400		
Phe	Lys	Lys	Pro	Met	Gly	Ser	Trp	Glu	Cys	Thr	Val	Cys	His	Met	Gln		
				405					410					415			
Asn	Lys	Thr	Glu	Asp	Asn	Thr	Cys	Val	Gly	Cys	Lys	Ala	Glu	Lys	Pro		
			420					425					430				
Gly	Thr	Val	Lys	Ser	Val	Pro	Thr	Ala	Ala	Pro	Ser	Gly	Leu	Leu	Gly		
		435					440					445					
Leu	Leu	His	Gln	Phe	Lys	Lys	Pro	Thr	Gly	Ser	Trp	Asp	Cys	Asp	Val		
	450					455					460						
Cys	Leu	Ile	Gln	Asn	Lys	Pro	Glu	Ala	Ala	Lys	Cys	Ile	Ala	Cys	Glu		
465					470					475					480		
Ser	Ala	Lys	Pro	Gly	Thr	Lys	Ala	Glu	Pro	Lys	Gly	Thr	Phe	Asp	Thr		
				485					490					495			
Val	Lys	Asn	Ser	Val	Ser	Val	Ala	Pro	Leu	Ser	Ser	Gly	Gln	Leu	Gly		
			500					505					510				
Leu	Leu	Asp	Gln	Phe	Lys	Lys	Ser	Ala	Gly	Ser	Trp	Asp	Cys	Asp	Val		
		515					520					525					
Cys	Leu	Val	Glu	Asn	Lys	Pro	Glu	Ala	Thr	Lys	Cys	Val	Ala	Cys	Glu		
	530					535					540						
Thr	Ser	Lys	Pro	Gly	Thr	Lys	Ala	Glu	Leu	Lys	Gly	Phe	Gly	Thr	Ser		
545					550					555					560		
Thr	Phe	Ser	Ser	Gly	Thr	Ala	Ala	Pro	Thr	Phe	Lys	Phe	Gly	Val	Gln		
				565					570					575			
Ser	Ser	Asp	Ser	Thr	Ala	Glu	Leu	Lys	Ser	Gly	Ala	Ser	Thr	Ser	Gly		
			580					585					590				
Phe	Ala	Lys	Ser	Ile	Gly	Asp	Phe	Lys	Phe	Gly	Leu	Val	Ser	Ala	Ser		
		595					600					605					
Thr	Thr	Thr	Glu	Glu	Thr	Gly	Lys	Lys	Ser	Phe	Thr	Phe	Gly	Ser	Ser		
	610					615					620						
Thr	Thr	Asn	Glu	Val	Ser	Ala	Gly	Phe	Lys	Phe	Gly	Ile	Ala	Gly	Ser		
625					630					635					640		
Ala	Gln	Thr	Lys	Pro	Asp	Thr	Leu	Ser	Gln	Ser	Thr	Thr	Ser	Gly	Phe		
				645					650					655			
Thr	Phe	Gly	Ser	Val	Ser	Asn	Thr	Val	Ser	Leu	Ala	Pro	Ala	Ala	Thr		
				660				665					670				
Ser	Ser	Ser	Ser	Thr	Gly	Leu	Gln	Val	Ala	Ala	Ala	Ile	Ala	Asp	Ser		
		675					680					685					
Asn	Leu	Ala	Thr	Thr	Ala	Ala	Leu	Lys	Ser	Ala	Glu	Lys	Lys	Ala			
	690					695						700					
Glu	Ala	Pro	Thr	Ile	Thr	Pro	Phe	Ser	Phe	Gly	Lys	Thr	Asp	Gln	Asn		
705					710					715					720		
Lys	Glu	Thr	Ala	Ser	Thr	Ser	Phe	Val	Phe	Gly	Lys	Lys	Asp	Glu	Lys		
				725					730					735			

ATTORNEY DOCKET 21101.0045U2

Thr Asp Ser Ala Pro Thr Gly Ser Ser Phe Ala Phe Gly Leu Lys Lys
 740 745 750
 Asp Gly Glu Glu Ser Lys Pro Phe Leu Phe Gly Lys Pro Glu Pro Thr
 755 760 765
 Lys Val Asp Gly Asn Ala Ala Ser Ala Gly Phe Ala Phe Gly Val Thr
 770 775 780
 Asn Pro Thr Glu Lys Lys Asp Ile Glu Gln Pro Gly Lys Ser Val Phe
 785 790 795 800
 Ala Phe Gly Ala Gln Thr Ser Ile Thr Asp Ala Gly Ala Ser Lys Gln
 805 810 815
 Pro Phe Ser Phe Leu Thr Asn Val Ser Ser Thr Ala Ala Ser Ser Ser
 820 825 830
 Thr Cys Gly Val Ser Ser Ser Val Phe Gly Ser Val Thr Gln Ser Ser
 835 840 845
 Thr Pro Ala Thr Pro Ser Asn Val Phe Gly Ser Ala Ile Ser Ala Asn
 850 855 860
 Ala Pro Ala Pro Ser Ser Gly Val Phe Gly Asn Leu Thr Pro Ser Asn
 865 870 875 880
 Ala Pro Ala Ala Ser Ser Thr Leu Phe Gly Asn Val Ala Pro Ser Ser
 885 890 895
 Thr Pro Ser Gly Ser Ser Gly Leu Phe Gly Thr Ala Ala Ala Ser Ser
 900 905 910
 Thr Pro Ala Thr Ser Thr Ser Leu Phe Gly Ser Ala Ala Lys Ser Ser
 915 920 925
 Ala Pro Ala Ser Ser Gly Gly Val Phe Asn Ser Ala Ala Pro Ala Ala
 930 935 940
 Pro Ala Ser Thr Thr Ser Ser Val Phe Gly Ser Val Ala Ser Ser Thr
 945 950 955 960
 Asn Thr Ser Ala Asn Ser Ala Asn Ile Phe Gly Ser Ser Gly Gly Ala
 965 970 975
 Ala Thr Ala Pro Gly Ala Phe Val Phe Gly Gln Pro Ala Ser Thr Ala
 980 985 990
 Ser Thr Val Phe Gly Asn Ser Ser Glu Ser Lys Ser Thr Phe Val Phe
 995 1000 1005
 Ser Gly Gln Glu Asn Lys Pro Val Thr Ser Ala Ser Thr Ser Val Thr
 1010 1015 1020
 Pro Phe Leu Phe Gly Ala Val Ser Ala Thr Thr Pro Ala Ala Pro
 1025 1030 1035 1040
 Ser Phe Asn Phe Gly Arg Thr Ile Thr Ser Asn Thr Thr Gly Thr Ser
 1045 1050 1055
 Ser Ser Pro Phe Ile Phe Gly Ala Gly Ala Ser Gly Ser Ala Ser Ser
 1060 1065 1070
 Ser Ile Thr Ala Gln Ala Asn Pro Val Pro Ala Phe Gly Gln Ser Ser
 1075 1080 1085
 Asn Pro Ser Thr Ala Pro Ala Phe Gly Ser Ser Thr Ser Val Pro Val
 1090 1095 1100
 Phe Pro Ala Gly Ser Ser Gln Gln Val Pro Ala Phe Gly Ser Ser Ser
 1105 1110 1115 1120
 Ala Gln Pro Pro Val Phe Gly Gln Gln Ala Ala Gln Pro Ser Phe Gly
 1125 1130 1135
 Ser Pro Ala Ala Pro Ser Ala Gly Ser Gly Phe Pro Phe Gly Asn Asn
 1140 1145 1150
 Ala Asn Phe Asn Phe Asn Ser Thr Asn Ser Ser Gly Gly Val Phe Thr
 1155 1160 1165
 Phe Asn Ala Asn Ser Gly Ser Thr Thr Gln Pro Pro Pro Gly Tyr
 1170 1175 1180
 Met Phe Asn Ala Ala Ala Pro Gly Phe Asn Ile Gly Thr Asn Gly Arg
 1185 1190 1195 1200
 Thr Thr Pro Ala Ser Thr Ile Ser Thr Arg Lys Ile Lys Thr Ala Arg
 1205 1210 1215
 Arg Arg Lys

<210> 7
 <211> 10697
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 7
 cacagtgggc ctccgccggc tacggcgctg cgctactggg ttgcaggcgc tttcctcttg 60
 gaagtggcga ctgctgcggg cctgagcgct ggtctcagcg gcctcgggag ccaggttggc 120
 ggcgcgatga ggcgcagcaa ggctgacgtg gagcggtaca tcgcctcggg gcagggctcc 180
 accccgctcg ctgcacagaa gtcaatgaaa ggattctatt ttgcaaagct gtattatgaa 240
 gctaaagaat atgatcttgc taaaaaatat atatgtactt acattaatgt gcaagagagg 300
 gatcccaaag ctcacagatt tctgggtctt ctttatgaat tggaaagaaa cacagacaaa 360
 gccgttgaat gttacaggcg ttcagtggaa ttaaacccaa cacaaaaaga tcttgtgttg 420
 aagattgcag aattgctttg taaaaatgat gttactgatg gaagagcaaa atactggctt 480
 gaaagagcag ccaaactttt ccaggaagt cctgcaattt ataaactaaa ggaacagctt 540
 ctagattgtg aagggtgaaga tggatggaat aaactttttg acttgattca gtcagaactt 600
 tatgtaagac ctgatgacgt ccattgtgaac atccggctag tggaggtgta tcgctcaact 660
 aaaagattga aggatgctgt ggcccactgc catgaggcag agaggaacat agctttgcgt 720
 tcaagtttag aatggaattc gtgtgttgta cagaccctta aggaatatct ggagtcttta 780
 cagtgtttgg agtctgataa aagtgactgg cgagcaacca atacagactt actgctggcc 840
 tatgctaate ttatgcttct tacgctttcc actagagatg tgcaggaaaag tagagaatta 900
 ctgcaaagtt ttgatagtgc tcttcagtct gtgaaatctt tgggtggaaa tgatgaactg 960
 tcagctactt tcttagaaat gaaaggacat tctacatgc atgctgggtt tctgcttttg 1020
 aagatgggtc agcatagtag taatgttcaa tggcgagctc tttctgagct ggctgcattg 1080
 tgctatctca tagcatttca ggttccaaga ccaaagatta aattaataaa aggtgaagct 1140
 ggacaaaatc tgctggaaat gatggcctgt gaccgactga gccaatcagg gcacatgttg 1200
 ctaaacttaa gtcgtggcaa gcaagatttt taaaagaga ttggtgaaac ttttgccaac 1260
 aaaagcgggc agtctgcatt atatgatgct ctgttttcta gtcagtcacc taaggataca 1320
 tcttttcttg gtagcgatga tattggaaac attgatgtac gagaaccaga gcttgaagat 1380
 ttgactagat acgatgttggt tgctattcga gcacataatg gtagtcttca gcaccttact 1440
 tggcttggct tacagtggaa ttcattgcct gctttacctg gaatccgaaa atggctaaaa 1500
 cagcttttcc atcatttgcc ccattgaaac tcaaggcttg aaacaaatgc acctgaatca 1560
 atatgtatct tagatcttga agtatttctc cttggagtag tatataccag ccacttacia 1620
 ttaaaggaga aatgtaattc tcaccacagc tcctatcagc cgttatgcct gcccttctct 1680
 gtgtgtaaac agctttgtac agaaagacaa aaatcttggg gggatgcggg ttgtactctg 1740
 attcacagaa aagcagtacc tggaaacgta gcaaaattga gacttctagt tcagcatgaa 1800
 ataaacactc taagagccca ggaaaaacat ggccttcaac ctgctctgct tgtacattgg 1860
 gcagaatgcc ttcagaaaac gggcagcggg cttaattctt tttatgatca acgagaatac 1920
 ataggggaga gtgttcatta ttggaagaaa gttttgccat tgttgaagat aataaaaaag 1980
 aagaacagta ttctgaacc tattgatcct ctgttttaac attttcatag ttagacatt 2040
 caggcatcag aaattgttga atatgaagaa gacgcacaca taacttttgc tatattggat 2100
 gcagtaaatg gaaatataga agatgctgtg actgcttttg aatctataaa aagtgttggt 2160
 tcttatttga atcttgcaat gattttttcac aggaaggcag aagacattga aaatgatgcc 2220
 ctttctcttg aagaacaaga agaatgcaaa aattatctga gaaagaccag ggactacct 2280
 ataaagatta tagatgacag tgattcaaat ctttcagtgg tcaagaaatt gcctgtgcc 2340
 ctggagtctg taaaagagat gcttaattca gtcatgcagg aactcgaaga ctatagttaa 2400
 ggaggtctct tctataaaaa tggttctttg cgaaatgcag attcagaaat aaaacattct 2460
 acaccgtctc ctaccaaata ttcactatca ccaagtaaaa gttacaagta ttctcccaa 2520
 acaccacctc gatgggcaga agatcagaat tctttactga aaatgatttg ccaacaagta 2580
 gaggccatta agaaagaaat gcaggagtgt aaactaaata gcagtaactc agcatcccct 2640
 catcggttgg ccacagagaa ttatggacca gactcggtgc ctgatggata tcaggggtca 2700
 cagacatttc atggggctcc actaacagtt gcaactactg gcccttcagt atattatagt 2760
 cagtcaccag catataattc ccagtatctt ctcagaccag cagctaattg tactcccaca 2820
 aagggcccag tctatggcat gaataggctt ccaccccaac agcatattta tgcctatccg 2880
 caacagatgc acacaccgcc agtgcaaagc tcatctgctt gtatgttctc tcaggagatg 2940

tatggtcctc	ctgcattgcg	ttttgagtct	cctgcaacgg	gaattctatc	gcccaggggt	3000
gatgattact	ttaattacaa	tgttcaacag	acaagcacia	atccaccttt	gccagaacca	3060
ggatattttc	taaaacctcc	gattgcagct	catgcttcaa	gatctgcaga	atctaagact	3120
atagaatttg	ggaaaactaa	ttttgttcag	cccatgccgg	gtgaaggatt	aaggccatct	3180
ttgccaacac	aagcacacac	aacacagcca	actcctttta	aattttaactc	aaattttcaaa	3240
tcaaatgatg	gtgacttcac	gttttctctca	ccacagggttg	tgacacagcc	ccctcctgca	3300
gcttacagta	acagtgaag	ccttttaggt	ctcctgactt	cagataaacc	cttgcaagga	3360
gatggctata	gtggagccaa	accaattcct	ggtggtcaaa	ccattggggc	tcgaaatata	3420
ttcaattttg	gaagcaaaaa	tgtgtctgga	atttcattta	cagaaaaacat	ggggtcgagt	3480
cagcaaaaaga	attctgggtt	tcggcggaagt	gatgatatgt	ttactttcca	tggtccaggg	3540
aaatcagtat	ttggaacacc	cacttttagag	acagcaaaaca	agaatcatga	gacagatgga	3600
ggaagtggcc	atggggatga	tgatgatgac	ggtcctcact	ttgagcctgt	agtacctctt	3660
cctgataaga	ttgaagttaa	aactgggtgag	gaagatgaag	aagaattcctt	ttgcaaccgc	3720
gcgaaattgt	ttcgtttcga	tgtagaatcc	aaagaatgga	aagaacgtgg	gattggcaat	3780
gtaaaaatac	tgaggcataa	aacatctggt	aaaattcgcc	ttctaataag	acgagagcaa	3840
gtattgaaaa	tctgtgcaaa	tcattacatc	agtccagata	tgaaattgac	accaaagtct	3900
ggatcagaca	gatcttttgt	atggcatgcc	cttgattatg	cagatgagtt	gccaaaacca	3960
gaacaacttg	ctattagggt	caaaactcct	gaggaagcag	cacttttttaa	atgcaagttt	4020
gaagaagccc	agagcatttt	aaaagcccca	ggaacaaatg	tagccatggc	gtcaaatacag	4080
gctgtcagaa	ttgtaaaaaga	acccacaagt	catgataaca	aggatatttg	caaatactgat	4140
gctggaaacc	tgaattttga	atttcaggtt	gcaagaaaag	aagggtccttg	gtggcattgt	4200
aacagctgct	cattaaagaa	tgcttcaact	gctaagaaat	gtgtatcatg	ccaaatacta	4260
aaccaagca	ataaagagct	cgttggccca	ccattagctg	aaactgtttt	tactcctaaa	4320
accagcccag	agaatgttca	agatcgattt	gcattgggtga	ctccaaagaa	agaagggtcac	4380
tgggattgta	gtattttgtt	agtaagaaat	gaacctactg	tatctagggtg	cattgcgtgt	4440
cagaatacaa	aatctgctaa	caaaagtgga	tcttcatttg	ttcatcaagc	ttcattttaa	4500
tttggccagg	gagatcttcc	taaacctatt	aacagtgatt	tcagatctgt	tttttctaca	4560
aaggaaggac	agtgggattg	cagtgcattg	ttggtacaaa	atgaggggag	ctctacaaaa	4620
tgtctgtctt	gtcagaatcc	gagaaaacag	agtcctacctg	ctacttctat	tccaacacct	4680
gcctctttta	agtgttggtac	ttcagagaca	agtaaaactc	taaaaagtgg	atttgaagac	4740
atgttttgcta	agaaggaagg	acagtgggat	tgcagttcat	gcttagtgcg	aaatgaagca	4800
aatgctacaa	gatgtgttgc	ttgtcagaat	ccggataaac	caagtccatc	tacttctgtt	4860
ccagctcctg	cctcttttaa	gtttggtact	tcagagacaa	gcaaggctcc	aaagagcgga	4920
tttgagggaa	tgttcactaa	gaaggaggga	cagtgggatt	gcagtgtgtg	cttagtaaga	4980
aatgaagcca	gtgctaccaa	atgtattgct	tgtcagaatc	caggtaaaca	aatcaaaact	5040
acttctgcag	tttcaacacc	tgccctcttca	gagacaagca	aggctccaaa	gagcggattt	5100
gaggaatgt	tcactaagaa	ggagggacag	tgggattgca	gtgtgtgtct	agtaagaaat	5160
gaagccagtg	ctaccaaagt	tattgcttgt	cagaatccag	gtaaacaaaa	tcaaactact	5220
tctgcagttt	caacacctgc	ctcttcagag	acaaggaagg	ctccaaagag	cggattttgag	5280
ggaatgttca	ctaagaagga	aggacagtg	gattgcaagt	tgtgcttagt	aagaaatgaa	5340
gccagtgtca	ccaaatgtat	tgcttgtcag	tgtccaaagta	aacaaaatca	aacaactgca	5400
atttcaacac	ctgcctcttc	ggagataagc	aagggtccaa	agagtggatt	tgaaggaatg	5460
ttcatcagga	aaggacagtg	ggattgtagt	gtttgctgtg	tacaaaatga	gagttcttcc	5520
ttaaaatgtg	tggcttgtga	tgccctctaaa	ccaactcata	aacctattgc	agaagctcct	5580
tcagctttca	cactgggctc	agaaatgaag	ttgcatgact	cttctggaag	tcagggtggga	5640
acaggattta	aaagtaattt	ctcagaaaaa	gcttctaagt	ttggcaatac	agagcaagga	5700
ttcaaatttg	ggcatgtgga	tcaagaaaaa	tcaccttcat	ttatgtttca	gggttcttct	5760
aatacagaat	ttaagtcaac	caaagaagga	ttttccatcc	ctgtgtctgc	tgatggattt	5820
aaattttggca	tttcggaacc	aggaaatcaa	gaaaagaaaa	gtgaaaagcc	tcttgaaaaa	5880
ggtactggct	tccaggctca	ggatattagt	ggccagaaga	atggccgtgg	tgtgattttt	5940
ggccaaacaa	gtagcacttt	tacatttgca	gatcttgcaa	aatcaacttc	aggagaagga	6000
tttcagtttg	gcaaaaaaga	ccccaatctc	aagggttttt	cagggtgctg	agaaaaatta	6060
ttctcatcac	aatacggtaa	aatggccaat	aaagcaaaaca	cttccgggtga	ctttgagaaa	6120
gatgatgatg	cctataagac	tgaggacagc	gatgacatcc	attttgaacc	agtagttcaa	6180
atgcccgaag	aagtagaact	tgtaacagga	gaagaagatg	aaaaagttct	gtattcacag	6240
cgggtaaaaa	tatttagatt	tgatgctgag	gtaagtcagt	ggaaagaaag	gggcttgggg	6300
aacttaaaaa	ttctcaaaaa	cgaggctaat	ggcaaaactaa	gaatgctgat	gcgaagagaa	6360
caagtactaa	aagtgtgtgc	taatcattgg	ataacgacta	cgatgaacct	gaagcctctc	6420
tctggatcag	atagagcatg	gatgtgggtt	gccagtgatt	tctctgatgg	tgatgcaaaa	6480
ctagagcagt	tggcagcaaa	atttaaaaca	ccagagctgg	ctgaagaatt	caagcagaaa	6540
tttgaggaat	gccagcggct	tctgttagac	ataccacttc	aaactcccca	taaacttgta	6600

gatactggca	gagctgccaa	gttaatacag	agagctgaag	aaatgaagag	tggactgaaa	6660
gatttcaaaa	cattttttgac	aaatgatcaa	acaaaagtca	ctgaggaaga	aaataagggt	6720
tcaggtacag	gtgcgccgg	tgccctcagac	acaacaataa	aacccaatcc	tgaaaacact	6780
gggcccacat	tagaatggga	taactatgat	ttaagggaag	atgcttttga	tgatagtgtc	6840
agtagtagct	cagtacatgc	ttctccattg	gcaagtagcc	ctgtgagaaa	aaatcttttc	6900
cgttttggtg	agtcaacaac	aggatttaac	ttcagtttta	aatctgcttt	gagtccatct	6960
aagtctcctg	ccaagttgaa	tcagagtggg	acttcagttg	gcactgatga	agaatctgat	7020
gttactcaag	aagaagagag	agatggacag	tactttgaac	ctgttgttcc	tttacctgat	7080
ctagttagag	tatccagtg	tgaggaaaat	gaacaagttg	tttttagtca	cagggcaaaa	7140
ctctacagat	atgataaaga	tgttggtcaa	tggaagaaa	ggggcattgg	tgatataaag	7200
attttacaga	attatgataa	taagcaagtt	cgtatagtga	tgagaaggga	ccaagtatta	7260
aaactttgtg	ccaatcacag	aataactcca	gacatgactt	tgcaaaatat	gaaagggaca	7320
gaaagagtat	ggttggtggac	tgcatgtgat	tttgcatagt	gagaaagaaa	agtagagcat	7380
ttagctgttc	gttttaaaact	acaggatggt	gcagactcgt	ttaagaaaat	ttttgatgaa	7440
gcaaaaacag	cccaggaaaa	agatttctttg	ataacacctc	atgtttctcg	gtcaagcact	7500
cccagagagt	caccatgtgg	caaaattgct	gtagctgtat	tagaagaaac	cacaagagag	7560
aggacagatg	ttattcaggg	tgatgatgta	gcagatgcaa	cttcagaagt	tgaagtgtct	7620
agcacatctg	aaacaacacc	aaaagcagtg	gtttctcctc	caaagtttgt	atttggttca	7680
gagctctgta	aaagcatttt	tagtagtgaa	aaatcaaaac	catttgcatt	cggcaacagt	7740
tcagccactg	ggtctttgtt	tggttttagt	tttaatgcac	ctttgaaaag	taacaatagt	7800
gaaactagtt	cagtagccca	gagtggatct	gaaagcaaa	tggaacctaa	aaaatgtgaa	7860
ctgtcaaaga	actctgatat	cgaacagtct	tcagatagca	aagtcaaaaa	tctctttgct	7920
tcctttccaa	cggagaatc	ttcaatcaac	tacacattta	aaacaccaga	aaaggcaaaa	7980
gagaagaaaa	aacctgaaga	ttctccctca	gatgatgatg	ttctcattgt	atatgaacta	8040
actccaaccg	ctgagcagaa	agcccttgca	accaaactta	aacttctctc	aactttcttc	8100
tgctacaaga	atagaccaga	ttatgttagt	gaagaagagg	aggatgatga	agatttcgaa	8160
acagctgtca	agaaacttaa	tggaaaacta	tatttggtatg	gctcagaaaa	atgtagacct	8220
ttggaagaaa	atacagcaga	taatgagaaa	gaatgtatta	ttgtttggga	aaagaaacca	8280
acagttgaag	agaaggcaaa	agcagatagc	ttaaaacttc	cacctacatt	tttttgtgga	8340
gtctgtagt	atactgatga	agacaatgga	aatggggaag	actttcaatc	agagcttcaa	8400
aaagttcagg	aagctcaaaa	atctcagaca	gaagaaataa	ctagcacaa	tgacagtgt	8460
tatacagggtg	ggactgaagt	gatggtacct	tctttctgta	aatctgaaga	acctgattct	8520
attaccaaat	ccattagttc	accatctgtt	tctctgaaa	ctatggacaa	acctgtagat	8580
ttgtcaacta	gaaaggaaat	tgatacagat	tctacaagcc	aaggggaaag	caagatagtt	8640
tcatttggtg	ttggaagtag	cacagggctc	tcatttgtag	acttggtctc	cagtaattct	8700
ggagattttg	cttttggttc	taaagataaa	aatttccaat	gggcaaatac	tggagcagct	8760
gtgtttggaa	cacagtcagt	cggaaaccag	tcagccggt	aagttggtga	agatgaagat	8820
ggtagtgatg	aagaagtagt	tcataatgaa	gatattccatt	ttgaaccaat	agtgtcacta	8880
cagaggttag	aagtaaaatc	tggaagaaga	gatgaagaaa	ttttgtttaa	agagagagcc	8940
aaactttata	gatgggtagc	ggatgtcagt	cagtggaagg	agcgcggtgt	tggagatata	9000
aagattcttt	ggcatacaat	gaagaattat	taccggatcc	taatgagaag	agaccagggt	9060
tttaaagtgt	gtgcaaacca	cgttattact	aaaacaatgg	aattaaagcc	cttaaagtgt	9120
tcaataaatg	ctttagtttg	gactgcctca	gattatgctg	atggagaagc	aaaagtagaa	9180
cagcttgtag	tgagatttaa	aactaaagaa	gtagctgatt	gtttcaagaa	aacatttgaa	9240
gaatgtcagc	agaatttaat	gaaactccag	aaaggacatg	tatcactggc	agcagaatta	9300
tcaaaggaga	ccaatcctgt	ggtgtttttt	gatgtttgtg	cggacggtga	acctctaggg	9360
cggataacta	tgggaattatt	ttcaaacatt	gttctctcga	ctgctgagaa	cttcagagca	9420
ctatgcactg	gagagaaaag	ctttgggttc	aagaattcca	tttttcacag	agtaattcca	9480
gattttgttt	gccaaggagg	agatatcacc	aaacatgatg	gaacaggcgg	acagtccatt	9540
tatggagaca	aatttgaaga	tgaaaatttt	gatgtgaaac	atactgggtc	tggtttacta	9600
tccatggcca	atcaaggcca	gaataccaat	aattctcaat	ttgtttatac	actgaagaaa	9660
gcagaacatt	tggactttta	gcatgtagta	tttgggtttg	ttaaggatgg	catggatact	9720
gtgaaaaaga	ttgaatcatt	tggttctccc	aaagggtctg	tttgtcgaag	aataactatc	9780
acagaatgtg	gacagatata	aatcatttgt	tgttcataga	aaatttcata	tgtataagca	9840
gttggattga	agcttagcta	ttacaatttg	atagttatgt	tcagcttttg	aaaatggacg	9900
tttcgagatt	acaaatgtaa	aattgcagct	tatagctgtt	gtcacttttt	aatgtgttat	9960
aattgcacct	gcattggtgtg	aaataaaagt	ttaaactctg	gtgatttcag	gtgtacttgt	10020
gtttatgtac	tcttgacgta	ttaaaatgga	ataatactaa	tcttggttaa	agcaatagac	10080
ctcaaactat	tgaagggaata	tgatatatgc	aatttaattt	taattccttt	taagatattt	10140
ggacttctctg	catggatata	cttaccattt	gaataaagg	accacaactt	ggataattta	10200
atttttaggtt	tgaaatatat	ttggtaattct	taactattgg	tgtactcatt	tatgcataga	10260

gactcgttta tgaatgggta gagccacaga acgtatagag ttaaccaaag tgctcttctc 10320
 tagaatcttt acacctcctg tgtggttaca agttaacttt gtaagtagcg taccttcctt 10380
 ccttaaaata tctagcttcc tgtgcccttt catagatatt cgattaattt ttacatttta 10440

aacaagttga ctatttcctt taggggtttt gtttcaaact tttctgtcat ctgtctctac 10500
 tacctcagaa actgcagctt ggttctgatg atagaaattg aatttttcct tgtagttatt 10560
 gtgataaagt atgaatattt ttagaaaagtc tataccatgt tctttcgta aagatttgct 10620
 ttatacaaga ttgttgtagt acctttttct ggtaaatttt gtagcagaaa taaaatgaca 10680
 attcctaaga gccaaaa 10697

<210> 8

<211> 3224

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 8

Met	Arg	Arg	Ser	Lys	Ala	Asp	Val	Glu	Arg	Tyr	Ile	Ala	Ser	Val	Gln
1				5				10					15		
Gly	Ser	Thr	Pro	Ser	Pro	Arg	Gln	Lys	Ser	Met	Lys	Gly	Phe	Tyr	Phe
			20					25					30		
Ala	Lys	Leu	Tyr	Tyr	Glu	Ala	Lys	Glu	Tyr	Asp	Leu	Ala	Lys	Lys	Tyr
		35					40					45			
Ile	Cys	Thr	Tyr	Ile	Asn	Val	Gln	Glu	Arg	Asp	Pro	Lys	Ala	His	Arg
	50				55					60					
Phe	Leu	Gly	Leu	Leu	Tyr	Glu	Leu	Glu	Glu	Asn	Thr	Asp	Lys	Ala	Val
65					70					75					80
Glu	Cys	Tyr	Arg	Arg	Ser	Val	Glu	Leu	Asn	Pro	Thr	Gln	Lys	Asp	Leu
				85					90					95	
Val	Leu	Lys	Ile	Ala	Glu	Leu	Leu	Cys	Lys	Asn	Asp	Val	Thr	Asp	Gly
			100					105					110		
Arg	Ala	Lys	Tyr	Trp	Leu	Glu	Arg	Ala	Ala	Lys	Leu	Phe	Pro	Gly	Ser
	115					120						125			
Pro	Ala	Ile	Tyr	Lys	Leu	Lys	Glu	Gln	Leu	Leu	Asp	Cys	Glu	Gly	Glu
	130					135					140				
Asp	Gly	Trp	Asn	Lys	Leu	Phe	Asp	Leu	Ile	Gln	Ser	Glu	Leu	Tyr	Val
145				150					155						160
Arg	Pro	Asp	Asp	Val	His	Val	Asn	Ile	Arg	Leu	Val	Glu	Val	Tyr	Arg
			165				170							175	
Ser	Thr	Lys	Arg	Leu	Lys	Asp	Ala	Val	Ala	His	Cys	His	Glu	Ala	Glu
		180					185						190		
Arg	Asn	Ile	Ala	Leu	Arg	Ser	Ser	Leu	Glu	Trp	Asn	Ser	Cys	Val	Val
	195					200						205			
Gln	Thr	Leu	Lys	Glu	Tyr	Leu	Glu	Ser	Leu	Gln	Cys	Leu	Glu	Ser	Asp
	210					215					220				
Lys	Ser	Asp	Trp	Arg	Ala	Thr	Asn	Thr	Asp	Leu	Leu	Leu	Ala	Tyr	Ala
225					230				235						240
Asn	Leu	Met	Leu	Leu	Thr	Leu	Ser	Thr	Arg	Asp	Val	Gln	Glu	Ser	Arg
			245						250					255	
Glu	Leu	Leu	Gln	Ser	Phe	Asp	Ser	Ala	Leu	Gln	Ser	Val	Lys	Ser	Leu
		260					265						270		
Gly	Gly	Asn	Asp	Glu	Leu	Ser	Ala	Thr	Phe	Leu	Glu	Met	Lys	Gly	His
		275					280					285			
Phe	Tyr	Met	His	Ala	Gly	Ser	Leu	Leu	Leu	Lys	Met	Gly	Gln	His	Ser
	290					295					300				
Ser	Asn	Val	Gln	Trp	Arg	Ala	Leu	Ser	Glu	Leu	Ala	Ala	Leu	Cys	Tyr
305				310					315						320

Leu Ile Ala Phe Gln Val Pro Arg Pro Lys Ile Lys Leu Ile Lys Gly
 325 330 335
 Glu Ala Gly Gln Asn Leu Leu Glu Met Met Ala Cys Asp Arg Leu Ser
 340 345 350
 Gln Ser Gly His Met Leu Leu Asn Leu Ser Arg Gly Lys Gln Asp Phe
 355 360 365
 Leu Lys Glu Ile Val Glu Thr Phe Ala Asn Lys Ser Gly Gln Ser Ala
 370 375 380
 Leu Tyr Asp Ala Leu Phe Ser Ser Gln Ser Pro Lys Asp Thr Ser Phe
 385 390 395 400
 Leu Gly Ser Asp Asp Ile Gly Asn Ile Asp Val Arg Glu Pro Glu Leu
 405 410 415
 Glu Asp Leu Thr Arg Tyr Asp Val Gly Ala Ile Arg Ala His Asn Gly
 420 425 430
 Ser Leu Gln His Leu Thr Trp Leu Gly Leu Gln Trp Asn Ser Leu Pro
 435 440 445
 Ala Leu Pro Gly Ile Arg Lys Trp Leu Lys Gln Leu Phe His His Leu
 450 455 460
 Pro His Glu Thr Ser Arg Leu Glu Thr Asn Ala Pro Glu Ser Ile Cys
 465 470 475 480
 Ile Leu Asp Leu Glu Val Phe Leu Leu Gly Val Val Tyr Thr Ser His
 485 490 495
 Leu Gln Leu Lys Glu Lys Cys Asn Ser His His Ser Ser Tyr Gln Pro
 500 505 510
 Leu Cys Leu Pro Leu Pro Val Cys Lys Gln Leu Cys Thr Glu Arg Gln
 515 520 525
 Lys Ser Trp Trp Asp Ala Val Cys Thr Leu Ile His Arg Lys Ala Val
 530 535 540
 Pro Gly Asn Val Ala Lys Leu Arg Leu Leu Val Gln His Glu Ile Asn
 545 550 555 560
 Thr Leu Arg Ala Gln Glu Lys His Gly Leu Gln Pro Ala Leu Leu Val
 565 570 575
 His Trp Ala Glu Cys Leu Gln Lys Thr Gly Ser Gly Leu Asn Ser Phe
 580 585 590
 Tyr Asp Gln Arg Glu Tyr Ile Gly Arg Ser Val His Tyr Trp Lys Lys
 595 600 605
 Val Leu Pro Leu Leu Lys Ile Ile Lys Lys Lys Asn Ser Ile Pro Glu
 610 615 620
 Pro Ile Asp Pro Leu Phe Lys His Phe His Ser Val Asp Ile Gln Ala
 625 630 635 640
 Ser Glu Ile Val Glu Tyr Glu Glu Asp Ala His Ile Thr Phe Ala Ile
 645 650 655
 Leu Asp Ala Val Asn Gly Asn Ile Glu Asp Ala Val Thr Ala Phe Glu
 660 665 670
 Ser Ile Lys Ser Val Val Ser Tyr Trp Asn Leu Ala Leu Ile Phe His
 675 680 685
 Arg Lys Ala Glu Asp Ile Glu Asn Asp Ala Leu Ser Pro Glu Glu Gln
 690 695 700
 Glu Glu Cys Lys Asn Tyr Leu Arg Lys Thr Arg Asp Tyr Leu Ile Lys
 705 710 715 720
 Ile Ile Asp Asp Ser Asp Ser Asn Leu Ser Val Val Lys Lys Leu Pro
 725 730 735
 Val Pro Leu Glu Ser Val Lys Glu Met Leu Asn Ser Val Met Gln Glu
 740 745 750
 Leu Glu Asp Tyr Ser Glu Gly Gly Pro Leu Tyr Lys Asn Gly Ser Leu
 755 760 765
 Arg Asn Ala Asp Ser Glu Ile Lys His Ser Thr Pro Ser Pro Thr Lys
 770 775 780
 Tyr Ser Leu Ser Pro Ser Lys Ser Tyr Lys Tyr Ser Pro Lys Thr Pro
 785 790 795 800

Pro	Arg	Trp	Ala	Glu	Asp	Gln	Asn	Ser	Leu	Leu	Lys	Met	Ile	Cys	Gln	
				805					810					815		
Gln	Val	Glu	Ala	Ile	Lys	Lys	Glu	Met	Gln	Glu	Leu	Lys	Leu	Asn	Ser	
			820					825					830			
Ser	Asn	Ser	Ala	Ser	Pro	His	Arg	Trp	Pro	Thr	Glu	Asn	Tyr	Gly	Pro	
		835					840					845				
Asp	Ser	Val	Pro	Asp	Gly	Tyr	Gln	Gly	Ser	Gln	Thr	Phe	His	Gly	Ala	
	850					855					860					
Pro	Leu	Thr	Val	Ala	Thr	Thr	Gly	Pro	Ser	Val	Tyr	Tyr	Ser	Gln	Ser	
865					870					875					880	
Pro	Ala	Tyr	Asn	Ser	Gln	Tyr	Leu	Leu	Arg	Pro	Ala	Ala	Asn	Val	Thr	
			885						890					895		
Pro	Thr	Lys	Gly	Pro	Val	Tyr	Gly	Met	Asn	Arg	Leu	Pro	Pro	Gln	Gln	
		900						905						910		
His	Ile	Tyr	Ala	Tyr	Pro	Gln	Gln	Met	His	Thr	Pro	Pro	Val	Gln	Ser	
	915						920					925				
Ser	Ser	Ala	Cys	Met	Phe	Ser	Gln	Glu	Met	Tyr	Gly	Pro	Pro	Ala	Leu	
	930					935					940					
Arg	Phe	Glu	Ser	Pro	Ala	Thr	Gly	Ile	Leu	Ser	Pro	Arg	Gly	Asp	Asp	
945					950					955					960	
Tyr	Phe	Asn	Tyr	Asn	Val	Gln	Gln	Thr	Ser	Thr	Asn	Pro	Pro	Leu	Pro	
			965						970					975		
Glu	Pro	Gly	Tyr	Phe	Thr	Lys	Pro	Pro	Ile	Ala	Ala	His	Ala	Ser	Arg	
		980					985						990			
Ser	Ala	Glu	Ser	Lys	Thr	Ile	Glu	Phe	Gly	Lys	Thr	Asn	Phe	Val	Gln	
	995						1000					1005				
Pro	Met	Pro	Gly	Glu	Gly	Leu	Arg	Pro	Ser	Leu	Pro	Thr	Gln	Ala	His	
	1010					1015					1020					
Thr	Thr	Gln	Pro	Thr	Pro	Phe	Lys	Phe	Asn	Ser	Asn	Phe	Lys	Ser	Asn	
1025					1030					1035					1040	
Asp	Gly	Asp	Phe	Thr	Phe	Ser	Ser	Pro	Gln	Val	Val	Thr	Gln	Pro	Pro	
			1045						1050					1055		
Pro	Ala	Ala	Tyr	Ser	Asn	Ser	Glu	Ser	Leu	Leu	Gly	Leu	Leu	Thr	Ser	
		1060					1065					1070				
Asp	Lys	Pro	Leu	Gln	Gly	Asp	Gly	Tyr	Ser	Gly	Ala	Lys	Pro	Ile	Pro	
	1075					1080					1085					
Gly	Gly	Gln	Thr	Ile	Gly	Pro	Arg	Asn	Thr	Phe	Asn	Phe	Gly	Ser	Lys	
	1090					1095					1100					
Asn	Val	Ser	Gly	Ile	Ser	Phe	Thr	Glu	Asn	Met	Gly	Ser	Ser	Gln	Gln	
1105					1110					1115					1120	
Lys	Asn	Ser	Gly	Phe	Arg	Arg	Ser	Asp	Asp	Met	Phe	Thr	Phe	His	Gly	
			1125						1130					1135		
Pro	Gly	Lys	Ser	Val	Phe	Gly	Thr	Pro	Thr	Leu	Glu	Thr	Ala	Asn	Lys	
		1140					1145						1150			
Asn	His	Glu	Thr	Asp	Gly	Gly	Ser	Ala	His	Gly	Asp	Asp	Asp	Asp	Asp	
	1155					1160					1165					
Gly	Pro	His	Phe	Glu	Pro	Val	Val	Pro	Leu	Pro	Asp	Lys	Ile	Glu	Val	
	1170				1175						1180					
Lys	Thr	Gly	Glu	Glu	Asp	Glu	Glu	Glu	Phe	Phe	Cys	Asn	Arg	Ala	Lys	
1185					1190					1195					1200	
Leu	Phe	Arg	Phe	Asp	Val	Glu	Ser	Lys	Glu	Trp	Lys	Glu	Arg	Gly	Ile	
			1205						1210					1215		
Gly	Asn	Val	Lys	Ile	Leu	Arg	His	Lys	Thr	Ser	Gly	Lys	Ile	Arg	Leu	
		1220					1225						1230			
Leu	Met	Arg	Arg	Glu	Gln	Val	Leu	Lys	Ile	Cys	Ala	Asn	His	Tyr	Ile	
		1235					1240					1245				
Ser	Pro	Asp	Met	Lys	Leu	Thr	Pro	Asn	Ala	Gly	Ser	Asp	Arg	Ser	Phe	
	1250					1255					1260					
Val	Trp	His	Ala	Leu	Asp	Tyr	Ala	Asp	Glu	Leu	Pro	Lys	Pro	Glu	Gln	
1265					1270					1275					1280	

Leu Ala Ile Arg Phe Lys Thr Pro Glu Glu Ala Ala Leu Phe Lys Cys
 1285 1290 1295
 Lys Phe Glu Glu Ala Gln Ser Ile Leu Lys Ala Pro Gly Thr Asn Val
 1300 1305 1310
 Ala Met Ala Ser Asn Gln Ala Val Arg Ile Val Lys Glu Pro Thr Ser
 1315 1320 1325
 His Asp Asn Lys Asp Ile Cys Lys Ser Asp Ala Gly Asn Leu Asn Phe
 1330 1335 1340
 Glu Phe Gln Val Ala Lys Lys Glu Gly Ser Trp Trp His Cys Asn Ser
 1345 1350 1355 1360
 Cys Ser Leu Lys Asn Ala Ser Thr Ala Lys Lys Cys Val Ser Cys Gln
 1365 1370 1375
 Asn Leu Asn Pro Ser Asn Lys Glu Leu Val Gly Pro Pro Leu Ala Glu
 1380 1385 1390
 Thr Val Phe Thr Pro Lys Thr Ser Pro Glu Asn Val Gln Asp Arg Phe
 1395 1400 1405
 Ala Leu Val Thr Pro Lys Lys Glu Gly His Trp Asp Cys Ser Ile Cys
 1410 1415 1420
 Leu Val Arg Asn Glu Pro Thr Val Ser Arg Cys Ile Ala Cys Gln Asn
 1425 1430 1435 1440
 Thr Lys Ser Ala Asn Lys Ser Gly Ser Ser Phe Val His Gln Ala Ser
 1445 1450 1455
 Phe Lys Phe Gly Gln Gly Asp Leu Pro Lys Pro Ile Asn Ser Asp Phe
 1460 1465 1470
 Arg Ser Val Phe Ser Thr Lys Glu Gly Gln Trp Asp Cys Ser Ala Cys
 1475 1480 1485
 Leu Val Gln Asn Glu Gly Ser Ser Thr Lys Cys Ala Ala Cys Gln Asn
 1490 1495 1500
 Pro Arg Lys Gln Ser Leu Pro Ala Thr Ser Ile Pro Thr Pro Ala Ser
 1505 1510 1515 1520
 Phe Lys Phe Gly Thr Ser Glu Thr Ser Lys Thr Leu Lys Ser Gly Phe
 1525 1530 1535
 Glu Asp Met Phe Ala Lys Lys Glu Gly Gln Trp Asp Cys Ser Ser Cys
 1540 1545 1550
 Leu Val Arg Asn Glu Ala Asn Ala Thr Arg Cys Val Ala Cys Gln Asn
 1555 1560 1565
 Pro Asp Lys Pro Ser Pro Ser Thr Ser Val Pro Ala Pro Ala Ser Phe
 1570 1575 1580
 Lys Phe Gly Thr Ser Glu Thr Ser Lys Ala Pro Lys Ser Gly Phe Glu
 1585 1590 1595 1600
 Gly Met Phe Thr Lys Lys Glu Gly Gln Trp Asp Cys Ser Val Cys Leu
 1605 1610 1615
 Val Arg Asn Glu Ala Ser Ala Thr Lys Cys Ile Ala Cys Gln Asn Pro
 1620 1625 1630
 Gly Lys Gln Asn Gln Thr Thr Ser Ala Val Ser Thr Pro Ala Ser Ser
 1635 1640 1645
 Glu Thr Ser Lys Ala Pro Lys Ser Gly Phe Glu Gly Met Phe Thr Lys
 1650 1655 1660
 Lys Glu Gly Gln Trp Asp Cys Ser Val Cys Leu Val Arg Asn Glu Ala
 1665 1670 1675 1680
 Ser Ala Thr Lys Cys Ile Ala Cys Gln Asn Pro Gly Lys Gln Asn Gln
 1685 1690 1695
 Thr Thr Ser Ala Val Ser Thr Pro Ala Ser Ser Glu Thr Ser Lys Ala
 1700 1705 1710
 Pro Lys Ser Gly Phe Glu Gly Met Phe Thr Lys Lys Glu Gly Gln Trp
 1715 1720 1725
 Asp Cys Ser Val Cys Leu Val Arg Asn Glu Ala Ser Ala Thr Lys Cys
 1730 1735 1740
 Ile Ala Cys Gln Cys Pro Ser Lys Gln Asn Gln Thr Thr Ala Ile Ser
 1745 1750 1755 1760

Thr Pro Ala Ser Ser Glu Ile Ser Lys Ala Pro Lys Ser Gly Phe Glu
 1765 1770 1775
 Gly Met Phe Ile Arg Lys Gly Gln Trp Asp Cys Ser Val Cys Cys Val
 1780 1785 1790
 Gln Asn Glu Ser Ser Ser Leu Lys Cys Val Ala Cys Asp Ala Ser Lys
 1795 1800 1805
 Pro Thr His Lys Pro Ile Ala Glu Ala Pro Ser Ala Phe Thr Leu Gly
 1810 1815 1820
 Ser Glu Met Lys Leu His Asp Ser Ser Gly Ser Gln Val Gly Thr Gly
 1825 1830 1835 1840
 Phe Lys Ser Asn Phe Ser Glu Lys Ala Ser Lys Phe Gly Asn Thr Glu
 1845 1850 1855
 Gln Gly Phe Lys Phe Gly His Val Asp Gln Glu Asn Ser Pro Ser Phe
 1860 1865 1870
 Met Phe Gln Gly Ser Ser Asn Thr Glu Phe Lys Ser Thr Lys Glu Gly
 1875 1880 1885
 Phe Ser Ile Pro Val Ser Ala Asp Gly Phe Lys Phe Gly Ile Ser Glu
 1890 1895 1900
 Pro Gly Asn Gln Glu Lys Lys Ser Glu Lys Pro Leu Glu Asn Gly Thr
 1905 1910 1915 1920
 Gly Phe Gln Ala Gln Asp Ile Ser Gly Gln Lys Asn Gly Arg Gly Val
 1925 1930 1935
 Ile Phe Gly Gln Thr Ser Ser Thr Phe Thr Phe Ala Asp Leu Ala Lys
 1940 1945 1950
 Ser Thr Ser Gly Glu Gly Phe Gln Phe Gly Lys Lys Asp Pro Asn Phe
 1955 1960 1965
 Lys Gly Phe Ser Gly Ala Gly Glu Lys Leu Phe Ser Ser Gln Tyr Gly
 1970 1975 1980
 Lys Met Ala Asn Lys Ala Asn Thr Ser Gly Asp Phe Glu Lys Asp Asp
 1985 1990 1995 2000
 Asp Ala Tyr Lys Thr Glu Asp Ser Asp Asp Ile His Phe Glu Pro Val
 2005 2010 2015
 Val Gln Met Pro Glu Lys Val Glu Leu Val Thr Gly Glu Glu Asp Glu
 2020 2025 2030
 Lys Val Leu Tyr Ser Gln Arg Val Lys Leu Phe Arg Phe Asp Ala Glu
 2035 2040 2045
 Val Ser Gln Trp Lys Glu Arg Gly Leu Gly Asn Leu Lys Ile Leu Lys
 2050 2055 2060
 Asn Glu Val Asn Gly Lys Leu Arg Met Leu Met Arg Arg Glu Gln Val
 2065 2070 2075 2080
 Leu Lys Val Cys Ala Asn His Trp Ile Thr Thr Thr Met Asn Leu Lys
 2085 2090 2095
 Pro Leu Ser Gly Ser Asp Arg Ala Trp Met Trp Leu Ala Ser Asp Phe
 2100 2105 2110
 Ser Asp Gly Asp Ala Lys Leu Glu Gln Leu Ala Ala Lys Phe Lys Thr
 2115 2120 2125
 Pro Glu Leu Ala Glu Glu Phe Lys Gln Lys Phe Glu Glu Cys Gln Arg
 2130 2135 2140
 Leu Leu Leu Asp Ile Pro Leu Gln Thr Pro His Lys Leu Val Asp Thr
 2145 2150 2155 2160
 Gly Arg Ala Ala Lys Leu Ile Gln Arg Ala Glu Glu Met Lys Ser Gly
 2165 2170 2175
 Leu Lys Asp Phe Lys Thr Phe Leu Thr Asn Asp Gln Thr Lys Val Thr
 2180 2185 2190
 Glu Glu Glu Asn Lys Gly Ser Gly Thr Gly Ala Ala Gly Ala Ser Asp
 2195 2200 2205
 Thr Thr Ile Lys Pro Asn Pro Glu Asn Thr Gly Pro Thr Leu Glu Trp
 2210 2215 2220
 Asp Asn Tyr Asp Leu Arg Glu Asp Ala Leu Asp Asp Ser Val Ser Ser
 2225 2230 2235 2240

Ser Ser Val His Ala Ser Pro Leu Ala Ser Ser Pro Val Arg Lys Asn
 2245 2250 2255
 Leu Phe Arg Phe Gly Glu Ser Thr Thr Gly Phe Asn Phe Ser Phe Lys
 2260 2265 2270
 Ser Ala Leu Ser Pro Ser Lys Ser Pro Ala Lys Leu Asn Gln Ser Gly
 2275 2280 2285
 Thr Ser Val Gly Thr Asp Glu Glu Ser Asp Val Thr Gln Glu Glu Glu
 2290 2295 2300
 Arg Asp Gly Gln Tyr Phe Glu Pro Val Val Pro Leu Pro Asp Leu Val
 2305 2310 2315 2320
 Glu Val Ser Ser Gly Glu Glu Asn Glu Gln Val Val Phe Ser His Arg
 2325 2330 2335
 Ala Lys Leu Tyr Arg Tyr Asp Lys Asp Val Gly Gln Trp Lys Glu Arg
 2340 2345 2350
 Gly Ile Gly Asp Ile Lys Ile Leu Gln Asn Tyr Asp Asn Lys Gln Val
 2355 2360 2365
 Arg Ile Val Met Arg Arg Asp Gln Val Leu Lys Leu Cys Ala Asn His
 2370 2375 2380
 Arg Ile Thr Pro Asp Met Thr Leu Gln Asn Met Lys Gly Thr Glu Arg
 2385 2390 2395 2400
 Val Trp Leu Trp Thr Ala Cys Asp Phe Ala Asp Gly Glu Arg Lys Val
 2405 2410 2415
 Glu His Leu Ala Val Arg Phe Lys Leu Gln Asp Val Ala Asp Ser Phe
 2420 2425 2430
 Lys Lys Ile Phe Asp Glu Ala Lys Thr Ala Gln Glu Lys Asp Ser Leu
 2435 2440 2445
 Ile Thr Pro His Val Ser Arg Ser Ser Thr Pro Arg Glu Ser Pro Cys
 2450 2455 2460
 Gly Lys Ile Ala Val Ala Val Leu Glu Glu Thr Thr Arg Glu Arg Thr
 2465 2470 2475 2480
 Asp Val Ile Gln Gly Asp Asp Val Ala Asp Ala Thr Ser Glu Val Glu
 2485 2490 2495
 Val Ser Ser Thr Ser Glu Thr Thr Pro Lys Ala Val Val Ser Pro Pro
 2500 2505 2510
 Lys Phe Val Phe Gly Ser Glu Ser Val Lys Ser Ile Phe Ser Ser Glu
 2515 2520 2525
 Lys Ser Lys Pro Phe Ala Phe Gly Asn Ser Ser Ala Thr Gly Ser Leu
 2530 2535 2540
 Phe Gly Phe Ser Phe Asn Ala Pro Leu Lys Ser Asn Asn Ser Glu Thr
 2545 2550 2555 2560
 Ser Ser Val Ala Gln Ser Gly Ser Glu Ser Lys Val Glu Pro Lys Lys
 2565 2570 2575
 Cys Glu Leu Ser Lys Asn Ser Asp Ile Glu Gln Ser Ser Asp Ser Lys
 2580 2585 2590
 Val Lys Asn Leu Phe Ala Ser Phe Pro Thr Glu Glu Ser Ser Ile Asn
 2595 2600 2605
 Tyr Thr Phe Lys Thr Pro Glu Lys Ala Lys Glu Lys Lys Pro Glu
 2610 2615 2620
 Asp Ser Pro Ser Asp Asp Asp Val Leu Ile Val Tyr Glu Leu Thr Pro
 2625 2630 2635 2640
 Thr Ala Glu Gln Lys Ala Leu Ala Thr Lys Leu Lys Leu Pro Pro Thr
 2645 2650 2655
 Phe Phe Cys Tyr Lys Asn Arg Pro Asp Tyr Val Ser Glu Glu Glu Glu
 2660 2665 2670
 Asp Asp Glu Asp Phe Glu Thr Ala Val Lys Lys Leu Asn Gly Lys Leu
 2675 2680 2685
 Tyr Leu Asp Gly Ser Glu Lys Cys Arg Pro Leu Glu Glu Asn Thr Ala
 2690 2695 2700
 Asp Asn Glu Lys Glu Cys Ile Ile Val Trp Glu Lys Lys Pro Thr Val
 2705 2710 2715 2720

Glu Glu Lys Ala Lys Ala Asp Thr Leu Lys Leu Pro Pro Thr Phe Phe
 2725 2730 2735
 Cys Gly Val Cys Ser Asp Thr Asp Glu Asp Asn Gly Asn Gly Glu Asp
 2740 2745 2750
 Phe Gln Ser Glu Leu Gln Lys Val Gln Glu Ala Gln Lys Ser Gln Thr
 2755 2760 2765
 Glu Glu Ile Thr Ser Thr Thr Asp Ser Val Tyr Thr Gly Gly Thr Glu
 2770 2775 2780
 Val Met Val Pro Ser Phe Cys Lys Ser Glu Glu Pro Asp Ser Ile Thr
 2785 2790 2795 2800
 Lys Ser Ile Ser Ser Pro Ser Val Ser Ser Glu Thr Met Asp Lys Pro
 2805 2810 2815
 Val Asp Leu Ser Thr Arg Lys Glu Ile Asp Thr Asp Ser Thr Ser Gln
 2820 2825 2830
 Gly Glu Ser Lys Ile Val Ser Phe Gly Phe Gly Ser Ser Thr Gly Leu
 2835 2840 2845
 Ser Phe Ala Asp Leu Ala Ser Ser Asn Ser Gly Asp Phe Ala Phe Gly
 2850 2855 2860
 Ser Lys Asp Lys Asn Phe Gln Trp Ala Asn Thr Gly Ala Ala Val Phe
 2865 2870 2875 2880
 Gly Thr Gln Ser Val Gly Thr Gln Ser Ala Gly Lys Val Gly Glu Asp
 2885 2890 2895
 Glu Asp Gly Ser Asp Glu Glu Val Val His Asn Glu Asp Ile His Phe
 2900 2905 2910
 Glu Pro Ile Val Ser Leu Pro Glu Val Glu Val Lys Ser Gly Glu Glu
 2915 2920 2925
 Asp Glu Glu Ile Leu Phe Lys Glu Arg Ala Lys Leu Tyr Arg Trp Asp
 2930 2935 2940
 Arg Asp Val Ser Gln Trp Lys Glu Arg Gly Val Gly Asp Ile Lys Ile
 2945 2950 2955 2960
 Leu Trp His Thr Met Lys Asn Tyr Tyr Arg Ile Leu Met Arg Arg Asp
 2965 2970 2975
 Gln Val Phe Lys Val Cys Ala Asn His Val Ile Thr Lys Thr Met Glu
 2980 2985 2990
 Leu Lys Pro Leu Asn Val Ser Asn Asn Ala Leu Val Trp Thr Ala Ser
 2995 3000 3005
 Asp Tyr Ala Asp Gly Glu Ala Lys Val Glu Gln Leu Ala Val Arg Phe
 3010 3015 3020
 Lys Thr Lys Glu Val Ala Asp Cys Phe Lys Lys Thr Phe Glu Glu Cys
 3025 3030 3035 3040
 Gln Gln Asn Leu Met Lys Leu Gln Lys Gly His Val Ser Leu Ala Ala
 3045 3050 3055
 Glu Leu Ser Lys Glu Thr Asn Pro Val Val Phe Phe Asp Val Cys Ala
 3060 3065 3070
 Asp Gly Glu Pro Leu Gly Arg Ile Thr Met Glu Leu Phe Ser Asn Ile
 3075 3080 3085
 Val Pro Arg Thr Ala Glu Asn Phe Arg Ala Leu Cys Thr Gly Glu Lys
 3090 3095 3100
 Gly Phe Gly Phe Lys Asn Ser Ile Phe His Arg Val Ile Pro Asp Phe
 3105 3110 3115 3120
 Val Cys Gln Gly Gly Asp Ile Thr Lys His Asp Gly Thr Gly Gly Gln
 3125 3130 3135
 Ser Ile Tyr Gly Asp Lys Phe Glu Asp Glu Asn Phe Asp Val Lys His
 3140 3145 3150
 Thr Gly Pro Gly Leu Leu Ser Met Ala Asn Gln Gly Gln Asn Thr Asn
 3155 3160 3165
 Asn Ser Gln Phe Val Ile Thr Leu Lys Lys Ala Glu His Leu Asp Phe
 3170 3175 3180
 Lys His Val Val Phe Gly Phe Val Lys Asp Gly Met Asp Thr Val Lys
 3185 3190 3195 3200

ATTORNEY DOCKET 21101.0045U2

Lys Ile Glu Ser Phe Gly Ser Pro Lys Gly Ser Val Cys Arg Arg Ile
 3205 3210 3215
 Thr Ile Thr Glu Cys Gly Gln Ile
 3220

<210> 9
 <211> 4346
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 9
 aagctggagc ggcgggtggcg gcggcgtagg gaggccgggg ccggggctga ggccgcggcc 60
 gggctctgcga ggccttggg gcggcaggcg gcggcgggcc ggggctcgag cccggaggca 120
 ggagcagccg ccatggccga gagcatcata attcgtgtcc agtccccaga tggagtgaag 180
 cggatcacag caacaaagag agaaacagca gcaacatttt tgaaaaaggt tgcaaaggag 240
 tttggcttcc aaaataatgg cttctcggtt tacatcaata gaaacaagac tggagagata 300
 acagcctcct ccaacaaatc cctcaacttg caaaaaatca agcatggcga tttgttggtc 360
 ctgtttccct cgagccttgc tgggcccctca tctgaaatgg agacgtcagt tccaccgggc 420
 ttcaaagtct ttggcgctcc caacgtggtg gaggatgaga ttgatcagta cctcagcaaa 480
 caggacggga agatttacag aagccgagac ccacagctat gccgccacgg ccctttgggg 540
 aaatgcgtgc actgcgtccc tctagagcca ttcgatgagg actatctaaa ccatctcgag 600
 cctcccgtga agcacatgtc cttccacgcc tacatccgga agctgactgg aggggctgac 660
 aaggggaagt ttgttgccct ggagaacatc agctgcaaga ttaagtcagg gtgcgagggg 720
 cacctcccgt ggccgaatgg catctgtact aagtgccagc cgagcgccat cacgctgaac 780
 agacagaagt acaggcatgt ggacaatatc atgtttgaga atcacaccgt cgctgaccgc 840
 tttcttgact tctggagaaa gacagggaac cagcaatttg ggtacttata cggacggtac 900
 accgagcaca aagacattcc ccttggcatc agggctgaag tggctgcgat ttatgagcca 960
 cctcagattg gtacacagaa cagcttggag cttcttgagg atccaaaagc tgaagtggtc 1020
 gatgaaattg ctgccaaact tggcctgcgg aaggttggct ggatatttac agacctcgtc 1080
 tcagaagata cccgaaaggg taccgtccgc tacagtcgaa ataaggacac ctatttccta 1140
 agttcagaag agtgcatac tgcaggagac ttccagaaca agcatcccaa catgtgccgg 1200
 ctctctccag acggacattt tggatccaag tttgttactg cagtggctac aggtggctct 1260
 gacaaccaag tccactttga agggatccag gtgtccaatc agtgtatggc actggtccgt 1320
 gatgagtgtt tgctgccatg caaggacgcc cggagcttg gctacgcaa ggagtctagc 1380
 agtgagcagt acgtgccga tgtgttttat aaggacgtag acaagtttgg caacgagatc 1440
 acccagctgg cccggcccct gcctgtggag tatctcatca tagacatac aacaactttc 1500
 cccaaggatc cagtttacac tttttctatt tcgcaaaatc catttcctat tgaaaaccgg 1560
 gatgtattgg gtgagacaca ggacttccat agcttggcca cctatttgtc tcagaatacc 1620
 tcatctgtgt tcttggtatc catctcagat ttccacctct tgcgtttcct ggtcaccaat 1680
 gaagttatgc ctctgcagga cagcatcagc ttgctgctgg aggccgtgcg gaccagaaat 1740
 gaggagctcg cccagacatg gaagaggtct gagcagtggg ccaccatcga gcagctgtgc 1800
 agtacagtgt gcgggcagct cccaggtctc catgagtacg gggccgtcga gggctccaca 1860
 cacacggcca ctgcagccat gtgggcctgt cagcactgca cgttcatgaa ccagccaggc 1920
 acaggccact gcgagatgtg cagcctcccc aggacctagg gcgcctgcc tctgctggct 1980
 aggaccgggc ccagcccagc ccttcctgaa gccagaagcg ttgctgagtg tgttccctgt 2040
 aactgcccc tagtgggcag ccctggagga acaaggggct ggctgtcctg ggctccctga 2100
 cccactgaag cttctcagca cgttcctccc tggagagcgg gcgccacggc tggattctg 2160
 caggctgaat gcagtctcca gactggaaac gcagagcggc tcctcacgcc taatcctgtt 2220
 gacaagtccc ccgcctgtt ggaaagacct ctgcctcta cgtggcacct ggaattgggg 2280
 cgcacagggg ggggcggatg ctgccaccac ccagccttct ctttattttc agtgcttttt 2340
 gtttgccct cctgccccca tgtttttctg gctgggagct cttggttacc ccctgtctg 2400
 actgcttggt ggaaggcacc ctgcctgtga gggccacttt cctctctag tagctgtgt 2460
 ctggtgggga cgcagtggcc ctggacacgg ctcccctctg caggtctgca ggtcgggtttg 2520
 ctgcctgccc tctcctctc acccgatgtc caggtgggat tttaaagtct gcattggtta 2580
 taacaacagt tatcagtaat tctgcccag aagactttta tttatttttt ttttaagataa 2640
 aaactgcaca aaaggggagt gagagagact agtttcaca tccttcctc ctttagtgaa 2700
 gccccgagg ttgtgtccag ggtgatgagt gtggacgggg gcaccagtca gttctccctt 2760

```

gaagtaaacc tcagtgcctg agacttttct accaagccac acagctgcag caactgcaga 2820
tactgcgggc tgcagcaggag cagtgggtggc gcctgccctg aggctgccct gcgatggcct 2880
gggtggggaga gctgggtcac cggtgccgat gctctggccc tccccaatat gctgcttcgt 2940
cccactgcac cgcctggctg agggcgtag gggctgtgcc tcttgtgagg gccatttggg 3000
acctccctgg ggcactgcac aattgatagt gtaccaatag ggggagactg ggcgatctgg 3060
aacagcacgt ggtgggggtcc tgcttgtgtg ctctgcgttc ctctgtggcg tggccaggcc 3120
ggggcctggc tcttaccggg ggagtgggtg gcattctcgat gcttctttgc cttaatgatg 3180
gccacatctg ggctgctctg caccacggg agaggctggc ccagctgcag actgcttagg 3240
gactttctgtg tccatcctgg ggggtaagcc cacgtgaccc acattcttgg cactatgaac 3300
agagaacatt tgctgttggt cttctgaagt ggtcagggcc atggctgaca cctccagggtc 3360
cgcttggcat gggacaccaa gtggaaggcc caagcagctc atctgctctt gggaccaggg 3420
gccagttggg ttgggtctgg tcacggcaga gcttttgtgg agggtcagga aggggtggaga 3480
ggagctgggt tgaagcggag tgctgcggat gcaactccca gcttgcccac cgcgggctgt 3540
ctgctctccc tcctagcagc tgtcacactg aagttttgtc ctctgctgtc tcctctgggtc 3600
ctgagatgag ctgtgagcct aggtggccaa ggcttctctg attgcttccc tgtgagtcca 3660
aggccttccc ccaccactgg gcagaggctg gacagcacgg acttctagag agagccgcgt 3720
tgccagttcc tctcccactc gctcgtcctt atccaccacg ctattatagt ttccgttgtc 3780
ctccaccagc atttccctta ctctgaagtt ccggcattca catcattcat gttttctttt 3840
gtcttttagc taaaggaaaa gcattggcga tttgtctgat tctggttttg agttactctt 3900
tgttcagtaa tgcactttat tttattgtcc aaagagagtc agagctaagc atacaggctt 3960
gggggtgagc cctgctgtga gagttcaggg cctgggaggg tcagccacct cctcttgtgg 4020
gaaggaggtc tcagccccac ctgcgcatct cactgccct tggtgtggac acaccctctc 4080
atgctaccag caccataatc cagtgggggt gactgggtgc acacctgccc aggtgaacac 4140
agcggctgcc agtctcctgg tcccagagg aggtggggcc tggccctggc tccctccaac 4200
cagctgctcc tgggacacag gtgctcctgc ttcggctctg tttcggctca caggtgtgca 4260
tcaactgggt tggatttgca ttacattgac cccagccctg cagtggaacc taataaaagc 4320
gcctgaagca aaaaaaaaaa aaaaaa 4346

```

<210> 10

<211> 608

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 10

```

Met Ala Glu Ser Ile Ile Ile Arg Val Gln Ser Pro Asp Gly Val Lys
 1           5           10           15
Arg Ile Thr Ala Thr Lys Arg Glu Thr Ala Ala Thr Phe Leu Lys Lys

          20           25           30
Val Ala Lys Glu Phe Gly Phe Gln Asn Asn Gly Phe Ser Val Tyr Ile
          35           40           45
Asn Arg Asn Lys Thr Gly Glu Ile Thr Ala Ser Ser Asn Lys Ser Leu
          50           55           60
Asn Leu Leu Lys Ile Lys His Gly Asp Leu Leu Phe Leu Phe Pro Ser
          65           70           75           80
Ser Leu Ala Gly Pro Ser Ser Glu Met Glu Thr Ser Val Pro Pro Gly
          85           90           95
Phe Lys Val Phe Gly Ala Pro Asn Val Val Glu Asp Glu Ile Asp Gln
          100          105          110
Tyr Leu Ser Lys Gln Asp Gly Lys Ile Tyr Arg Ser Arg Asp Pro Gln
          115          120          125
Leu Cys Arg His Gly Pro Leu Gly Lys Cys Val His Cys Val Pro Leu
          130          135          140
Glu Pro Phe Asp Glu Asp Tyr Leu Asn His Leu Glu Pro Pro Val Lys
          145          150          155          160
His Met Ser Phe His Ala Tyr Ile Arg Lys Leu Thr Gly Gly Ala Asp
          165          170          175

```

Lys	Gly	Lys	Phe	Val	Ala	Leu	Glu	Asn	Ile	Ser	Cys	Lys	Ile	Lys	Ser	180	185	190
Gly	Cys	Glu	Gly	His	Leu	Pro	Trp	Pro	Asn	Gly	Ile	Cys	Thr	Lys	Cys	195	200	205
Gln	Pro	Ser	Ala	Ile	Thr	Leu	Asn	Arg	Gln	Lys	Tyr	Arg	His	Val	Asp	210	215	220
Asn	Ile	Met	Phe	Glu	Asn	His	Thr	Val	Ala	Asp	Arg	Phe	Leu	Asp	Phe	225	230	235
Trp	Arg	Lys	Thr	Gly	Asn	Gln	Gln	Phe	Gly	Tyr	Leu	Tyr	Gly	Arg	Tyr	245	250	255
Thr	Glu	His	Lys	Asp	Ile	Pro	Leu	Gly	Ile	Arg	Ala	Glu	Val	Ala	Ala	260	265	270
Ile	Tyr	Glu	Pro	Pro	Gln	Ile	Gly	Thr	Gln	Asn	Ser	Leu	Glu	Leu	Leu	275	280	285
Glu	Asp	Pro	Lys	Ala	Glu	Val	Val	Asp	Glu	Ile	Ala	Ala	Lys	Leu	Gly	290	295	300
Leu	Arg	Lys	Val	Gly	Trp	Ile	Phe	Thr	Asp	Leu	Val	Ser	Glu	Asp	Thr	305	310	315
Arg	Lys	Gly	Thr	Val	Arg	Tyr	Ser	Arg	Asn	Lys	Asp	Thr	Tyr	Phe	Leu	325	330	335
Ser	Ser	Glu	Glu	Cys	Ile	Thr	Ala	Gly	Asp	Phe	Gln	Asn	Lys	His	Pro	340	345	350
Asn	Met	Cys	Arg	Leu	Ser	Pro	Asp	Gly	His	Phe	Gly	Ser	Lys	Phe	Val	355	360	365
Thr	Ala	Val	Ala	Thr	Gly	Gly	Pro	Asp	Asn	Gln	Val	His	Phe	Glu	Gly	370	375	380
Tyr	Gln	Val	Ser	Asn	Gln	Cys	Met	Ala	Leu	Val	Arg	Asp	Glu	Cys	Leu	385	390	395
Leu	Pro	Cys	Lys	Asp	Ala	Pro	Glu	Leu	Gly	Tyr	Ala	Lys	Glu	Ser	Ser	405	410	415
Ser	Glu	Gln	Tyr	Val	Pro	Asp	Val	Phe	Tyr	Lys	Asp	Val	Asp	Lys	Phe	420	425	430
Gly	Asn	Glu	Ile	Thr	Gln	Leu	Ala	Arg	Pro	Leu	Pro	Val	Glu	Tyr	Leu	435	440	445
Ile	Ile	Asp	Ile	Thr	Thr	Thr	Phe	Pro	Lys	Asp	Pro	Val	Tyr	Thr	Phe	450	455	460
Ser	Ile	Ser	Gln	Asn	Pro	Phe	Pro	Ile	Glu	Asn	Arg	Asp	Val	Leu	Gly	465	470	475
Glu	Thr	Gln	Asp	Phe	His	Ser	Leu	Ala	Thr	Tyr	Leu	Ser	Gln	Asn	Thr	485	490	495
Ser	Ser	Val	Phe	Leu	Asp	Thr	Ile	Ser	Asp	Phe	His	Leu	Leu	Leu	Phe	500	505	510
Leu	Val	Thr	Asn	Glu	Val	Met	Pro	Leu	Gln	Asp	Ser	Ile	Ser	Leu	Leu	515	520	525
Leu	Glu	Ala	Val	Arg	Thr	Arg	Asn	Glu	Glu	Leu	Ala	Gln	Thr	Trp	Lys	530	535	540
Arg	Ser	Glu	Gln	Trp	Ala	Thr	Ile	Glu	Gln	Leu	Cys	Ser	Thr	Val	Gly	545	550	555
Gly	Gln	Leu	Pro	Gly	Leu	His	Glu	Tyr	Gly	Ala	Val	Glu	Gly	Ser	Thr	565	570	575
His	Thr	Ala	Thr	Ala	Ala	Met	Trp	Ala	Cys	Gln	His	Cys	Thr	Phe	Met	580	585	590
Asn	Gln	Pro	Gly	Thr	Gly	His	Cys	Glu	Met	Cys	Ser	Leu	Pro	Arg	Thr	595	600	605

<210> 11

<211> 3067

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 11

```

ggtgggttta tctcaaggcc tgagtagccg gtaacaaacg agggttcccg ggattggacc      60
gacgcaccat gcctctgcga cttgatataa aaagaaagct aactgctaga tctgatcgag      120
ttaagagtgt ggatctgcat cctacagagc catggatgtt ggcaagtctt tacaatggca      180
gtgtgtgtgt ttggaatcat gaaacacaga cactggtgaa gacatttgaa gtatgtgac      240
ttcctgttcg agctgcaaag tttgttgcaa ggaagaattg ggttgtgaca ggagcggatg      300
acatgcagat tagagtgttc aattacaata ctctggagag agttcatatg tttgaagcac      360
actcagacta cattcgctgt attgctgttc atccaaccca gcctttcatt ctaactagca      420
gtgatgacat gcttattaag ctctgggact gggataaaaa atggtcttgc tcacaagtgt      480
ttgaaggaca caccattat gttatgcaga ttgtgatcaa ccccaaagat aacaatcagt      540
ttgccagtgc ctctttggac aggactatca aggtgtggca gttgggctct tcgtcaccaa      600
acttcacttt ggaaggacat gagaaaggcg tgaattgcat tgattactac agtgggtggg      660
acaagccata cctcatttca ggtgcagatg accgtcttgt taaaatatgg gattatcaga      720
ataaaacatg tgtgcagaca ctggaaggac atgcccacaa tgtgtcttgt gccagctttc      780
atcctgagtt gccaatcatt atcacagggt cagaagatgg aacagtacgt atttggcatt      840
caagcaccta ccggtttgag agcacactga attatggaat ggagagggtg tgggtgcgtg      900
ccagtctaag aggggtcaaa aatgtcgctt tgggctatga tgaaggagag atcattgtta      960
agcttggctg ggaggaacct gccatgtcca tggatgccaa tggaaagata atttgggcca      1020
agcattcaga agtccagcag gccaacctaa aagcaatggg agatgctgaa attaaagatg      1080
gtgaaagatt gccactggca gtaaaggata tgggcagttg tgaaatatac cctcagacta      1140
ttcagcacia tcctaattgg cggtttgtgg tgggtgtgtg tgatggggag tatatcatct      1200
acacagcaat ggcattgaga aacaagagct ttggatctgc tcaggagttt gcatgggccc      1260
acgattcttc agagtatgca ataagagaga gcaacagcat tgtaaagata tttaaagaact      1320
ttaaggaaaa aaaatcattt aaaccagatt ttggagcaga aagtatctac ggcggtcttct      1380
tattgggagt cagatctgta aatggcttag ccttctatga ctgggacaat acagaactca      1440
tacgaagaat tgaaattcag cccaaacata ttttctggtc tgactctgga gagctagtct      1500
gtattgtctac tgaggaatca ttttttatcc ttaagtatct gtcagaaaaa gtcttggctg      1560
cacaggaaac acatgaggga gttactgaag atggcattga agatgccttt gaggttcttg      1620
gtgagattca ggaaattgtg aaaacagggc tttgggtagg cgattgcttc atttacacaa      1680
gttctgtgaa cagattaaat tattatgttg gaggagaaat agtcaccatt gccactttgg      1740
acaggacgat gtatctccta ggctacattc ctaaagacaa caggctttat ctgggggata      1800
aagaattgaa catcattagc tattccctgc tggtttcagt cctggaatac cagacagctg      1860
tcatgcggag ggacttttagc atggctgata aggtccttcc taccattcca aaagaacaga      1920
ggaccagagt tgcacacttt ttggaaaagc agggcttcaa gcagcaagct cttacagtat      1980
ccacagatcc tgagcatcgt tttgagcttg ctcttcagct tggagagtta aaaattgcac      2040
accagttagc agtggaaagc gagtgcgaac agaagtggaa acaacttgct gaacttgcca      2100
ttagtaaatg tcagtttggc ctagcccagg agtgccctga tcatgcacag gattatgggg      2160
gcctgctgct tttggccact gcctctggaa atgctaatat ggtgaacaag ctagcagagg      2220
gtgaggagag agatggcaaa aataatgttg cattcatgag ctacttttta cagggaagg      2280
ttgatgcctg cctagagctc ttaattagaa ctggacggct gccagaagct gccttcttgg      2340
cccgaactta cttaccagat caggtttcaa gggtagtgaa actctggaga gagaatctct      2400
caaaagtcaa tcagaaagca gcagaatccc ttgctgaccc aacagagtat gaaaacctgt      2460
tccttggtat aaaagaagcc tttgttgttg aagaatgggt gaaggaaaca catgctgatc      2520
tgtggccagc caaacaatac ccacttgta cgcacaaatga agagagaaat gtcattggaag      2580
agggaaaaga ctttcagccc tcaagatcta cagctcaaca ggaacttgat gggaaacctg      2640
cttctcctac tccggttatt gtggcctccc acacagccaa caaagaagaa aagagtttac      2700
tcgaactaga agtagatttg gataatttgg aattagaaga tattgacaca acagatatca      2760
atctggatga agatattttg gatgattgac tgtaattgct tccatttacc tgactaaaca      2820
gatcattatt atatataggt attgattgct accctgacca cagtgccttg gactatgaga      2880
aacttcttag atttttatat gtaaagtctg tggaccactg ggagcacaat gccacatca      2940
tcttaagaag agtttatgtg cagcatttaa atcactgtgt tttccttgtt aactaaaaca      3000
gacatgggct ttgatttttt tcatactatt agaccatata tcataaaacc ttttgaatta      3060
aaaaaaa

```

<210> 12

<211> 906

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 12

Met	Pro	Leu	Arg	Leu	Asp	Ile	Lys	Arg	Lys	Leu	Thr	Ala	Arg	Ser	Asp
1				5					10					15	
Arg	Val	Lys	Ser	Val	Asp	Leu	His	Pro	Thr	Glu	Pro	Trp	Met	Leu	Ala
		20						25					30		
Ser	Leu	Tyr	Asn	Gly	Ser	Val	Cys	Val	Trp	Asn	His	Glu	Thr	Gln	Thr
	35						40					45			
Leu	Val	Lys	Thr	Phe	Glu	Val	Cys	Asp	Leu	Pro	Val	Arg	Ala	Ala	Lys
	50					55					60				
Phe	Val	Ala	Arg	Lys	Asn	Trp	Val	Val	Thr	Gly	Ala	Asp	Asp	Met	Gln
65					70					75					80
Ile	Arg	Val	Phe	Asn	Tyr	Asn	Thr	Leu	Glu	Arg	Val	His	Met	Phe	Glu
			85						90					95	
Ala	His	Ser	Asp	Tyr	Ile	Arg	Cys	Ile	Ala	Val	His	Pro	Thr	Gln	Pro
			100					105						110	
Phe	Ile	Leu	Thr	Ser	Ser	Asp	Asp	Met	Leu	Ile	Lys	Leu	Trp	Asp	Trp
	115						120					125			
Asp	Lys	Lys	Trp	Ser	Cys	Ser	Gln	Val	Phe	Glu	Gly	His	Thr	His	Tyr
	130					135					140				
Val	Met	Gln	Ile	Val	Ile	Asn	Pro	Lys	Asp	Asn	Asn	Gln	Phe	Ala	Ser
145					150					155					160
Ala	Ser	Leu	Asp	Arg	Thr	Ile	Lys	Val	Trp	Gln	Leu	Gly	Ser	Ser	Ser
			165						170						175
Pro	Asn	Phe	Thr	Leu	Glu	Gly	His	Glu	Lys	Gly	Val	Asn	Cys	Ile	Asp
		180						185					190		
Tyr	Tyr	Ser	Gly	Gly	Asp	Lys	Pro	Tyr	Leu	Ile	Ser	Gly	Ala	Asp	Asp
	195						200					205			
Arg	Leu	Val	Lys	Ile	Trp	Asp	Tyr	Gln	Asn	Lys	Thr	Cys	Val	Gln	Thr
	210					215					220				
Leu	Glu	Gly	His	Ala	Gln	Asn	Val	Ser	Cys	Ala	Ser	Phe	His	Pro	Glu
225					230					235					240
Leu	Pro	Ile	Ile	Ile	Thr	Gly	Ser	Glu	Asp	Gly	Thr	Val	Arg	Ile	Trp
			245						250					255	
His	Ser	Ser	Thr	Tyr	Arg	Leu	Glu	Ser	Thr	Leu	Asn	Tyr	Gly	Met	Glu
			260					265					270		
Arg	Val	Trp	Cys	Val	Ala	Ser	Leu	Arg	Gly	Ser	Asn	Asn	Val	Ala	Leu
		275					280					285			
Gly	Tyr	Asp	Glu	Gly	Ser	Ile	Ile	Val	Lys	Leu	Gly	Arg	Glu	Glu	Pro
	290					295					300				
Ala	Met	Ser	Met	Asp	Ala	Asn	Gly	Lys	Ile	Ile	Trp	Ala	Lys	His	Ser
305					310					315					320
Glu	Val	Gln	Gln	Ala	Asn	Leu	Lys	Ala	Met	Gly	Asp	Ala	Glu	Ile	Lys
			325						330					335	
Asp	Gly	Glu	Arg	Leu	Pro	Leu	Ala	Val	Lys	Asp	Met	Gly	Ser	Cys	Glu
		340					345						350		
Ile	Tyr	Pro	Gln	Thr	Ile	Gln	His	Asn	Pro	Asn	Gly	Arg	Phe	Val	Val
	355					360						365			
Val	Cys	Gly	Asp	Gly	Glu	Tyr	Ile	Ile	Tyr	Thr	Ala	Met	Ala	Leu	Arg
	370					375					380				
Asn	Lys	Ser	Phe	Gly	Ser	Ala	Gln	Glu	Phe	Ala	Trp	Ala	His	Asp	Ser
385					390					395					400
Ser	Glu	Tyr	Ala	Ile	Arg	Glu	Ser	Asn	Ser	Ile	Val	Lys	Ile	Phe	Lys
			405						410					415	
Asn	Phe	Lys	Glu	Lys	Lys	Ser	Phe	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ser
			420					425					430		

Ile Tyr Gly Gly Phe Leu Leu Gly Val Arg Ser Val Asn Gly Leu Ala
 435 440 445
 Phe Tyr Asp Trp Asp Asn Thr Glu Leu Ile Arg Arg Ile Glu Ile Gln
 450 455 460
 Pro Lys His Ile Phe Trp Ser Asp Ser Gly Glu Leu Val Cys Ile Ala
 465 470 475 480
 Thr Glu Glu Ser Phe Phe Ile Leu Lys Tyr Leu Ser Glu Lys Val Leu
 485 490 495
 Ala Ala Gln Glu Thr His Glu Gly Val Thr Glu Asp Gly Ile Glu Asp
 500 505 510
 Ala Phe Glu Val Leu Gly Glu Ile Gln Glu Ile Val Lys Thr Gly Leu
 515 520 525
 Trp Val Gly Asp Cys Phe Ile Tyr Thr Ser Ser Val Asn Arg Leu Asn
 530 535 540
 Tyr Tyr Val Gly Gly Glu Ile Val Thr Ile Ala His Leu Asp Arg Thr
 545 550 555 560
 Met Tyr Leu Leu Gly Tyr Ile Pro Lys Asp Asn Arg Leu Tyr Leu Gly
 565 570 575
 Asp Lys Glu Leu Asn Ile Ile Ser Tyr Ser Leu Leu Val Ser Val Leu
 580 585 590
 Glu Tyr Gln Thr Ala Val Met Arg Arg Asp Phe Ser Met Ala Asp Lys
 595 600 605
 Val Leu Pro Thr Ile Pro Lys Glu Gln Arg Thr Arg Val Ala His Phe
 610 615 620
 Leu Glu Lys Gln Gly Phe Lys Gln Gln Ala Leu Thr Val Ser Thr Asp
 625 630 635 640
 Pro Glu His Arg Phe Glu Leu Ala Leu Gln Leu Gly Glu Leu Lys Ile
 645 650 655
 Ala Tyr Gln Leu Ala Val Glu Ala Glu Ser Glu Gln Lys Trp Lys Gln
 660 665 670
 Leu Ala Glu Leu Ala Ile Ser Lys Cys Gln Phe Gly Leu Ala Gln Glu
 675 680 685
 Cys Leu His His Ala Gln Asp Tyr Gly Gly Leu Leu Leu Leu Ala Thr
 690 695 700
 Ala Ser Gly Asn Ala Asn Met Val Asn Lys Leu Ala Glu Gly Ala Glu
 705 710 715 720
 Arg Asp Gly Lys Asn Asn Val Ala Phe Met Ser Tyr Phe Leu Gln Gly
 725 730 735
 Lys Val Asp Ala Cys Leu Glu Leu Leu Ile Arg Thr Gly Arg Leu Pro
 740 745 750
 Glu Ala Ala Phe Leu Ala Arg Thr Tyr Leu Pro Ser Gln Val Ser Arg
 755 760 765
 Val Val Lys Leu Trp Arg Glu Asn Leu Ser Lys Val Asn Gln Lys Ala
 770 775 780
 Ala Glu Ser Leu Ala Asp Pro Thr Glu Tyr Glu Asn Leu Phe Pro Gly
 785 790 795 800
 Leu Lys Glu Ala Phe Val Val Glu Glu Trp Val Lys Glu Thr His Ala
 805 810 815
 Asp Leu Trp Pro Ala Lys Gln Tyr Pro Leu Val Thr Pro Asn Glu Glu
 820 825 830
 Arg Asn Val Met Glu Glu Gly Lys Asp Phe Gln Pro Ser Arg Ser Thr
 835 840 845
 Ala Gln Gln Glu Leu Asp Gly Lys Pro Ala Ser Pro Thr Pro Val Ile
 850 855 860
 Val Ala Ser His Thr Ala Asn Lys Glu Glu Lys Ser Leu Leu Glu Leu
 865 870 875 880
 Glu Val Asp Leu Asp Asn Leu Glu Leu Glu Asp Ile Asp Thr Thr Asp
 885 890 895
 Ile Asn Leu Asp Glu Asp Ile Leu Asp Asp
 900 905

<210> 13
 <211> 914
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

```

<400> 13
ggcggcgagc ggaatgcagc ggcccaggc ctggccacgt ccgcacccgg gggagggggc      60
cgcgcgggcc caggccgggg gcccggcgcc gcctgctcga gccggggagc cctcggggct      120
gcggttgagc gaaccttccc tctacaccat caaggctgtt ttcacctag ataatgacgg      180
gcgcgggctg ctggccaagt attatgatga cacattcccc tccatgaagg agcagatggt      240
tttcgagaaa aatgtcttca acaagaccag cggactgag agtgagattg catttttttg      300
gggtatgacc atcgtctaca agaacagcat tgacctcttc ctatacgtgg tgggctcatc      360
ctacgagaat gagctgatgc tcatgtctgt tctcacctgc ctgtttgagt ctctgaacca      420
catgttaagg aagaacgtgg agaagcgctg gttgctggag aacatggacg gagccttctt      480
ggtgctggac gagattgtgg atggcggtgt gattctggag agtgaccccc agcaagtgat      540
ccagaagggt aatttttagg cagatgatgg cggcttgact gaacagagtg tggcccagg      600
tcttcagttc gccaaaggaac aaattaaatg gtcgttattg aaatgaaggc tgtggattca      660
aggctccctg cccccagac catttcccca atcctggcaa aagcccaaag atcccagggt      720
caggagagac ccctctgtat cccaggtcc ctcccagaac tgactcctaa ggtctccagc      780
cagggttctt gagatgcaaa ggtttggcct caggagagtc accttttctc acggccctgg      840
ccttaactca tatcttaggc attcctggcc ccagggccct aataaacctg cttttgtctt      900
ctgcaaaaaa aaaa
ctgcaaaaaa aaaa      914
  
```

<210> 14
 <211> 210
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

```

<400> 14
Met Gln Arg Pro Glu Ala Trp Pro Arg Pro His Pro Gly Glu Gly Ala
1          5          10          15
Ala Ala Ala Gln Ala Gly Gly Pro Ala Pro Pro Ala Arg Ala Gly Glu
20          25          30
Pro Ser Gly Leu Arg Leu Gln Glu Pro Ser Leu Tyr Thr Ile Lys Ala
35          40          45
Val Phe Ile Leu Asp Asn Asp Gly Arg Arg Leu Leu Ala Lys Tyr Tyr
50          55          60
Asp Asp Thr Phe Pro Ser Met Lys Glu Gln Met Val Phe Glu Lys Asn
65          70          75          80
Val Phe Asn Lys Thr Ser Arg Thr Glu Ser Glu Ile Ala Phe Phe Gly
85          90          95
Gly Met Thr Ile Val Tyr Lys Asn Ser Ile Asp Leu Phe Leu Tyr Val
100         105         110
Val Gly Ser Ser Tyr Glu Asn Glu Leu Met Leu Met Ser Val Leu Thr
115         120         125
Cys Leu Phe Glu Ser Leu Asn His Met Leu Arg Lys Asn Val Glu Lys
130         135         140
Arg Trp Leu Leu Glu Asn Met Asp Gly Ala Phe Leu Val Leu Asp Glu
145         150         155         160
Ile Val Asp Gly Gly Val Ile Leu Glu Ser Asp Pro Gln Gln Val Ile
165         170         175
Gln Lys Val Asn Phe Arg Ala Asp Asp Gly Gly Leu Thr Glu Gln Ser
180         185         190
  
```

ATTORNEY DOCKET 21101.0045U2

Val Ala Gln Val Leu Gln Ser Ala Lys Glu Gln Ile Lys Trp Ser Leu
 195 200 205
 Leu Lys
 210

<210> 15

<211> 5064

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 15

gagaagggga	ccttcaggtc	caggcaaagg	gggaacttct	gtcgtgggaa	cgaaaaagaa	60
agaggattta	caggggtggg	ggacagaggg	gcagcaggaa	ccagaagggg	gacagtggcg	120
gtcgcaccgg	ggccgatccg	agagttcccc	ttagagaacg	gagctcacgg	gcggggaggc	180
ctcacctgct	agtaggacgc	agaaagacag	aaggcgaagg	agacccccctg	ccgtagccat	240
cttgccctctc	tgctgagcgg	aagcccccg	tcggctcctg	tctgttagcg	gcctctctag	300
gctaccactg	acaccgtctc	tgtggcccgg	agcctaagag	accggaagtt	cgtgtttcca	360
ggcgcttccg	gaaaccgcgg	gagagggtcg	ctgacgtgga	ggcgccgaa	gggcagcagg	420
gtgtgtcggg	gctcggatta	agacatcggg	gtcggagacc	tgagagatgt	taaccaaatt	480
cgagaccaag	agcgcgcggg	tcaaagggct	cagctttcac	cccaaaagac	cttggatcct	540
gactagttta	cataatgggg	tcatccagtt	atgggactat	cggatgtgca	ctctcattga	600
caagtttgat	gaacatgatg	gtccagtgcg	aggcattgac	ttccataagc	agcagccact	660
gttcgtctct	ggaggagatg	actataagat	taaggtttgg	aattacaagc	ttcggcgctg	720
tcttttcaca	ttgcttgggc	acttagatta	tattcgcacc	acgttttttc	atcatgaata	780
tccttgaggt	ctgagtgcct	ccgatgatca	gaccatccga	gtgtggaatt	ggcaatctag	840
aacctgtggt	tgtgtgttaa	cagggcacaa	ccattatgtg	atgtgtgctc	agttccaccc	900
cacagaagac	ttggtagtat	cagccagcct	ggaccagact	gtgcgcggtt	gggatatttc	960
tgggtctgagg	aaaaaaaaacc	tgtccctctg	tgcggtggaa	tcggatgtga	gaggaataac	1020
tgggggttgat	ctatttgga	ctacagatgc	agtgggtgaag	catgtactag	agggtcacga	1080
tcgtggagta	aactgggctg	ccttccaccc	cactatgccc	cttattgtat	ctggggcaga	1140
tgatcgtcaa	gtgaagatct	ggcgcacgaa	tgaatcaaag	gcacgggagg	ttgatacctg	1200
ccggggccat	tacaacaatg	tatcttgtgc	cgtcttccac	cctcgccaag	agttgatcct	1260
cagcaattct	gaggacaaga	gtattcgagt	ctgggatatg	tctaagcgga	ctgggggttca	1320
gacttttcgc	agagaccatg	atcgtttctg	ggtcctagct	gctcacccta	accttaacct	1380
ctttgcagca	ggccatgatg	gtggtatgat	tgtgtttaag	ctggaacggg	aacggccagc	1440
ctatgctggt	catggcaata	tgctacacta	tgtcaaggac	cgattcttac	gacagctgga	1500
tttcaacagc	tccaagatg	tagctgtgat	gcagttgcgg	agtggttcca	agtttccagt	1560
attcaatatg	tcataacaatc	cagcagaaaa	tgcagtcctg	ctttgtacaa	gagctagcaa	1620
tctagagaat	agtacctatg	acctgtacac	catccctaaa	gatgctgact	ccagaaatcc	1680
tgatgcgcct	gaaggggaaac	gatcctcagg	cctgacagcc	gtttgggtcg	ctcgaaatcg	1740
gtttgctgtc	ctagatcgga	tgcattcgct	tctgatcaag	aatctgaaga	atgagatcac	1800
caaaaaggta	caggtgccca	actgtgatga	gatcttctat	gctggcacag	gcaatctcct	1860
gcttcgagat	gcggactcta	tcacactctt	tgacgtacag	cagaagcgga	ctctggcatc	1920
tgtgaagatt	tctaaagtga	aatacgttat	ctggtcagca	gacatgtcac	atgtagcact	1980
actagccaaa	cacgccattg	tgatctgtaa	ccgcaactg	gatgctttat	gtaacattca	2040
tgagaacatt	cgtgtcaaga	gtggggcctg	ggatgagagt	ggggtattta	tctataccac	2100
aagcaaccac	atcaaatatg	ctgtcaccac	tggggaccac	gggatcattc	gaactctgga	2160
tttaccatc	tatgtcacac	gggtgaagg	caacaatgta	tactgcctag	acagggagtg	2220
tcgtccccgg	gtactcacca	ttgatccac	tgagttcaaa	ttcaagctgg	ccctgatcaa	2280
cagaaaatat	gatgaggtac	tgcacatgg	gaggaatgcc	aaactagttg	gccagtctat	2340
tattgcttat	ctccagaaga	agggtatcc	tgaagtggca	ctgcattttg	tcaaggatga	2400
gaaaactcgc	tttagtctgg	cactggagtg	tggaaacatt	gagattgctc	tggaagcagc	2460
caaagcactg	gatgacaaga	actgctggga	aaagctggga	gaagtggccc	tgctgcagg	2520
gaaccaccag	attgtggaaa	tgtgctatca	gcgtacaaaa	aactttgaca	aagtttcctt	2580
cctgtatctt	atcactggca	acttagaaaa	acttcgcaag	atgatgaaga	ttgctgagat	2640
cagaaaggac	atgagtggcc	actatcagaa	tgcctatcac	ctgggtgatg	tgctcagagc	2700
tgtgcggatc	ctgaagaact	gtggacagaa	gtccctggcc	tatctcacag	ctgctaccca	2760

```

tggcttagat gaagaagctg agagcctaaa ggagacattt gacccagaga aggagacaat 2820
cccagacatt gaccctaatt ccaagctgct ccagccacct gcacctatca tgccattgga 2880
taccaattgg cctttattga ctgtatccaa aggatttttt gaaggcacca ttgccagcaa 2940
agggaaggga ggagcactgg ctgctgacat tgacattgac actgttggtgta cagagggctg 3000
gggagaggat gcagagctgc agttggatga agatgggttt gtggaggcta cagaaggttt 3060
gggggatgat gctcttgcca agggacagga agaaggaggt ggctgggatg tagaagaaga 3120
tctggagctc cctcctgagc tggatatatc ccctggggca gctgggtggg ctgaagatgg 3180
tttctttgtg cccccaacca agggaacaag tccaactcag atctggtgta ataactctca 3240
gcttccagtt gatcacatcc tggcaggctc tttcgaaaca gccatgcggc tccttcatga 3300
ccaagtaggg gtaatccagt ttggccccta caagcaactg ttcctacaga catacgcccg 3360
aggccgcaca acctatcagg ctctgccttg cctaccctcc atgtatggct atcctaatcg 3420
caactggaag gatgcaggcg tgaagaatgg tgtaccagct gtgggcctga agcttaatga 3480
cctcatccaa cgggtgcagc tgtgctacca gctcaccaca gttggcaaat ttgaggaggc 3540
tgtggaaaaa ttccgttcca tccttctcag tgtgccactt cttgttgtgg acaataaaca 3600
agagattgca gaggccagc agctcatcac catttgccgt gagtacattg tgggtttgtc 3660
cgtggagaca gaaaggaaga agctgcccac agagactcta gaacagcaga agcgcatctg 3720
tgagatggca gcctatttca cccactcaaa cctgcagcct gtgcacatga tcctggtgct 3780
gcgtacagcc ctcaatctgt tcttcaagct caagaacttc aagacagctg ccacctttgc 3840
tcggcgcccta ctagaactcg ggcccagcc tgagggtggcc caacagaccc gaaaaatcct 3900
gtctgcctgt gagaagaatc ccacagatgc ctaccagctc aattatgaca tgcacaaccc 3960
ctttgacatt tgtgctgcat catatcggcc catctaccgt ggaaagccag tagaaaagtg 4020
tccactcagt ggggcctgct attcccctga gttcaaagggt caaatctgca gggtcaccac 4080
agtgcacagag attggcaaag atgtgattgg tttaaggatc agtcctctgc agtttcgcta 4140
aggccccctt tgtgtgcatg ggtcagtcac catatgttcc ccccagagaa tgtgtctata 4200
tcctccttct aacagcacct tccccctgca gctactcttc agatctggct ctctgtaccc 4260
taaaacctag tatctttttc tcttctatgg aaaatccgaa ggtctaaact tgactttttt 4320
gaggtcttct caacttgact acagttgtgc tcataattgt ccttgccttt ccagcttaat 4380
tattttaagg aacaaatgaa aactctgggc tgggtggagt ggctcatacc tgaatccca 4440
gcactttggg aggtcatcgg gggcagatca tctgaggcca ggagtccgag acctgcctgg 4500
ccaacatggc aacaccccgt ctctaataaa aatataaaaa ttagcctggc atggtagcat 4560
gcgcctatag tcccagctgc tcaggaggct gaggcattgag aatcgcttga acctaggagg 4620
tggaggttgc attcaactga gatcatacca cttcattcca gcctgggtga cagagcaaga 4680
ctctgtctca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaggaaaac tctgtgatgg 4740
acatttgttt agtaaattccc ttcagtattt atccctcctt tccccacagc agctttcttt 4800
cctgtcaact agaaaggagc aggatgtaat aaatacattt tgggtgtgact aggccacacc 4860
aactcttaat catctcccat tttccttaga catttaaaatt tcaaggcagg tacctctgt 4920
gtactcagaa atttgaagaa gttatttggg tttccaaaat gcacactgcg ggttattgat 4980
ttgttcttta caactattgt tctcatattt ctcacactaa ataaatctct atgagagctt 5040
cttgaaaaaa aaaaaaaaaa agcg 5064

```

<210> 16

<211> 1224

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 16

```

Met Leu Thr Lys Phe Glu Thr Lys Ser Ala Arg Val Lys Gly Leu Ser
 1             5             10             15
Phe His Pro Lys Arg Pro Trp Ile Leu Thr Ser Leu His Asn Gly Val
      20             25             30
Ile Gln Leu Trp Asp Tyr Arg Met Cys Thr Leu Ile Asp Lys Phe Asp
      35             40             45
Glu His Asp Gly Pro Val Arg Gly Ile Asp Phe His Lys Gln Gln Pro
      50             55             60
Leu Phe Val Ser Gly Gly Asp Asp Tyr Lys Ile Lys Val Trp Asn Tyr
65             70             75             80

```

Lys Leu Arg Arg Cys Leu Phe Thr Leu Leu Gly His Leu Asp Tyr Ile
 85 90 95
 Arg Thr Thr Phe Phe His His Glu Tyr Pro Trp Ile Leu Ser Ala Ser
 100 105 110
 Asp Asp Gln Thr Ile Arg Val Trp Asn Trp Gln Ser Arg Thr Cys Val
 115 120 125
 Cys Val Leu Thr Gly His Asn His Tyr Val Met Cys Ala Gln Phe His
 130 135 140
 Pro Thr Glu Asp Leu Val Val Ser Ala Ser Leu Asp Gln Thr Val Arg
 145 150 155 160
 Val Trp Asp Ile Ser Gly Leu Arg Lys Lys Asn Leu Ser Pro Gly Ala
 165 170 175
 Val Glu Ser Asp Val Arg Gly Ile Thr Gly Val Asp Leu Phe Gly Thr
 180 185 190
 Thr Asp Ala Val Val Lys His Val Leu Glu Gly His Asp Arg Gly Val
 195 200 205
 Asn Trp Ala Ala Phe His Pro Thr Met Pro Leu Ile Val Ser Gly Ala
 210 215 220
 Asp Asp Arg Gln Val Lys Ile Trp Arg Met Asn Glu Ser Lys Ala Trp
 225 230 235 240
 Glu Val Asp Thr Cys Arg Gly His Tyr Asn Asn Val Ser Cys Ala Val
 245 250 255
 Phe His Pro Arg Gln Glu Leu Ile Leu Ser Asn Ser Glu Asp Lys Ser
 260 265 270
 Ile Arg Val Trp Asp Met Ser Lys Arg Thr Gly Val Gln Thr Phe Arg
 275 280 285
 Arg Asp His Asp Arg Phe Trp Val Leu Ala Ala His Pro Asn Leu Asn
 290 295 300
 Leu Phe Ala Ala Gly His Asp Gly Gly Met Ile Val Phe Lys Leu Glu
 305 310 315 320
 Arg Glu Arg Pro Ala Tyr Ala Val His Gly Asn Met Leu His Tyr Val
 325 330 335
 Lys Asp Arg Phe Leu Arg Gln Leu Asp Phe Asn Ser Ser Lys Asp Val
 340 345 350
 Ala Val Met Gln Leu Arg Ser Gly Ser Lys Phe Pro Val Phe Asn Met
 355 360 365
 Ser Tyr Asn Pro Ala Glu Asn Ala Val Leu Leu Cys Thr Arg Ala Ser
 370 375 380
 Asn Leu Glu Asn Ser Thr Tyr Asp Leu Tyr Thr Ile Pro Lys Asp Ala
 385 390 395 400
 Asp Ser Gln Asn Pro Asp Ala Pro Glu Gly Lys Arg Ser Ser Gly Leu
 405 410 415
 Thr Ala Val Trp Val Ala Arg Asn Arg Phe Ala Val Leu Asp Arg Met
 420 425 430
 His Ser Leu Leu Ile Lys Asn Leu Lys Asn Glu Ile Thr Lys Lys Val
 435 440 445
 Gln Val Pro Asn Cys Asp Glu Ile Phe Tyr Ala Gly Thr Gly Asn Leu
 450 455 460
 Leu Leu Arg Asp Ala Asp Ser Ile Thr Leu Phe Asp Val Gln Gln Lys
 465 470 475 480
 Arg Thr Leu Ala Ser Val Lys Ile Ser Lys Val Lys Tyr Val Ile Trp
 485 490 495
 Ser Ala Asp Met Ser His Val Ala Leu Leu Ala Lys His Ala Ile Val
 500 505 510
 Ile Cys Asn Arg Lys Leu Asp Ala Leu Cys Asn Ile His Glu Asn Ile
 515 520 525
 Arg Val Lys Ser Gly Ala Trp Asp Glu Ser Gly Val Phe Ile Tyr Thr
 530 535 540
 Thr Ser Asn His Ile Lys Tyr Ala Val Thr Thr Gly Asp His Gly Ile
 545 550 555 560

```

Ile Arg Thr Leu Asp Leu Pro Ile Tyr Val Thr Arg Val Lys Gly Asn
565 570 575
Asn Val Tyr Cys Leu Asp Arg Glu Cys Arg Pro Arg Val Leu Thr Ile
580 585 590
Asp Pro Thr Glu Phe Lys Phe Lys Leu Ala Leu Ile Asn Arg Lys Tyr
595 600 605
Asp Glu Val Leu His Met Val Arg Asn Ala Lys Leu Val Gly Gln Ser
610 615 620
Ile Ile Ala Tyr Leu Gln Lys Lys Gly Tyr Pro Glu Val Ala Leu His
625 630 635 640
Phe Val Lys Asp Glu Lys Thr Arg Phe Ser Leu Ala Leu Glu Cys Gly
645 650 655
Asn Ile Glu Ile Ala Leu Glu Ala Ala Lys Ala Leu Asp Asp Lys Asn
660 665 670
Cys Trp Glu Lys Leu Gly Glu Val Ala Leu Leu Gln Gly Asn His Gln
675 680 685
Ile Val Glu Met Cys Tyr Gln Arg Thr Lys Asn Phe Asp Lys Val Ser
690 695 700
Phe Leu Tyr Leu Ile Thr Gly Asn Leu Glu Lys Leu Arg Lys Met Met
705 710 715 720
Lys Ile Ala Glu Ile Arg Lys Asp Met Ser Gly His Tyr Gln Asn Ala
725 730 735
Leu Tyr Leu Gly Asp Val Ser Glu Arg Val Arg Ile Leu Lys Asn Cys
740 745 750
Gly Gln Lys Ser Leu Ala Tyr Leu Thr Ala Ala Thr His Gly Leu Asp
755 760 765
Glu Glu Ala Glu Ser Leu Lys Glu Thr Phe Asp Pro Glu Lys Glu Thr
770 775 780
Ile Pro Asp Ile Asp Pro Asn Ala Lys Leu Leu Gln Pro Pro Ala Pro
785 790 795 800
Ile Met Pro Leu Asp Thr Asn Trp Pro Leu Leu Thr Val Ser Lys Gly
805 810 815
Phe Phe Glu Gly Thr Ile Ala Ser Lys Gly Lys Gly Gly Ala Leu Ala
820 825 830
Ala Asp Ile Asp Ile Asp Thr Val Gly Thr Glu Gly Trp Gly Glu Asp
835 840 845
Ala Glu Leu Gln Leu Asp Glu Asp Gly Phe Val Glu Ala Thr Glu Gly
850 855 860
Leu Gly Asp Asp Ala Leu Gly Lys Gly Gln Glu Glu Gly Gly Gly Trp
865 870 875 880
Asp Val Glu Glu Asp Leu Glu Leu Pro Pro Glu Leu Asp Ile Ser Pro
885 890 895
Gly Ala Ala Gly Gly Ala Glu Asp Gly Phe Phe Val Pro Pro Thr Lys
900 905 910
Gly Thr Ser Pro Thr Gln Ile Trp Cys Asn Asn Ser Gln Leu Pro Val
915 920 925
Asp His Ile Leu Ala Gly Ser Phe Glu Thr Ala Met Arg Leu Leu His
930 935 940
Asp Gln Val Gly Val Ile Gln Phe Gly Pro Tyr Lys Gln Leu Phe Leu
945 950 955 960
Gln Thr Tyr Ala Arg Gly Arg Thr Thr Tyr Gln Ala Leu Pro Cys Leu
965 970 975
Pro Ser Met Tyr Gly Tyr Pro Asn Arg Asn Trp Lys Asp Ala Gly Leu
980 985 990
Lys Asn Gly Val Pro Ala Val Gly Leu Lys Leu Asn Asp Leu Ile Gln
995 1000 1005
Arg Leu Gln Leu Cys Tyr Gln Leu Thr Thr Val Gly Lys Phe Glu Glu
1010 1015 1020
Ala Val Glu Lys Phe Arg Ser Ile Leu Leu Ser Val Pro Leu Leu Val
1025 1030 1035 1040

```


Val Asp Asn Lys Gln Glu Ile Ala Glu Ala Gln Gln Leu Ile Thr Ile
1045 1050 1055
Cys Arg Glu Tyr Ile Val Gly Leu Ser Val Glu Thr Glu Arg Lys Lys
1060 1065 1070
Leu Pro Lys Glu Thr Leu Glu Gln Gln Lys Arg Ile Cys Glu Met Ala
1075 1080 1085
Ala Tyr Phe Thr His Ser Asn Leu Gln Pro Val His Met Ile Leu Val
1090 1095 1100
Leu Arg Thr Ala Leu Asn Leu Phe Phe Lys Leu Lys Asn Phe Lys Thr
1105 1110 1115 1120
Ala Ala Thr Phe Ala Arg Arg Leu Leu Glu Leu Gly Pro Lys Pro Glu
1125 1130 1135
Val Ala Gln Gln Thr Arg Lys Ile Leu Ser Ala Cys Glu Lys Asn Pro
1140 1145 1150
Thr Asp Ala Tyr Gln Leu Asn Tyr Asp Met His Asn Pro Phe Asp Ile
1155 1160 1165
Cys Ala Ala Ser Tyr Arg Pro Ile Tyr Arg Gly Lys Pro Val Glu Lys
1170 1175 1180
Cys Pro Leu Ser Gly Ala Cys Tyr Ser Pro Glu Phe Lys Gly Gln Ile
1185 1190 1195 1200
Cys Arg Val Thr Thr Val Thr Glu Ile Gly Lys Asp Val Ile Gly Leu
1205 1210 1215
Arg Ile Ser Pro Leu Gln Phe Arg
1220

<210> 17

<211> 1208

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 17

ctggtgagaa	gacagcgaaa	tggcgccctcc	ggcccccggc	cgggcctccg	gcggctccgg	60
ggaggtagac	gagctgttcg	acgtaaagaa	cgctttctac	atcggcagct	accagcagtg	120
cataaacgag	gcgcagcggg	tgaagctgtc	aaagcccagag	agagacgtgg	agagggacgt	180
cttcctgtat	agagcgtacc	tggcgccagag	gaagttcggg	gtggtcctgg	atgagatcaa	240
gccctcctcg	gccccctgagc	tccaggccgt	gcgcatgttt	gctgactacc	tcgcccacga	300
gagtcggagg	gacagcatcg	tggccgagct	ggaccgagag	atgagcagga	gcgtggacgt	360
gaccaacacc	accttcctgc	tcattggccgc	ctccatctat	ctccacgacc	agaacccgga	420
tgcgcgccctg	cgtgcgctgc	accaggggga	cagcctggag	tcacacagcca	tgacagtgca	480
gatcctgctg	aagctggacc	gcctggacct	cgcccggag	gagctgaaga	gaatgcagga	540
cctggacgag	gatgccaccc	tcaccagct	cgccactgcc	tgggtcagcc	tggccacggg	600
tgggtgagaag	ctgcaggatg	cctactacat	cttcaggag	atggctgaca	agtgtcgcgc	660
cacctgctg	ctgctcaatg	ggcaggcggc	ctgccacatg	gccagggcc	gctgggaggc	720
cgctgagggc	ctgctgcagg	aggcgctaga	caaggatagt	ggctaccggg	agacgtgggt	780
caacctcatc	gtcctgtccc	agcacctggg	caagccccct	gaggtgacaa	accgatacct	840
gtcccagctg	aaggatgccc	acaggtccca	tcccttcac	aaggagtacc	aggccaagga	900
gaacgacttt	gacaggctgg	tgctacagta	cgctcccagc	gcctgaggct	ggcccagagc	960
tgtcaggacc	atgaagccag	gacagaggcc	aggagccagc	cctgcagccc	tccccacccg	1020
gcatccacct	gcatcccttc	tgggggcagg	agccccccc	cagcaccccc	atctgttaat	1080
aaatatctca	actccagggt	gttccacctg	aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	1140
aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	1200
aaaaaaaaa						1208

<210> 18

<211> 308

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 18

```

Met Ala Pro Pro Ala Pro Gly Pro Ala Ser Gly Gly Ser Gly Glu Val
 1           5           10           15
Asp Glu Leu Phe Asp Val Lys Asn Ala Phe Tyr Ile Gly Ser Tyr Gln
 20           25           30
Gln Cys Ile Asn Glu Ala Gln Arg Val Lys Leu Ser Ser Pro Glu Arg
 35           40           45
Asp Val Glu Arg Asp Val Phe Leu Tyr Arg Ala Tyr Leu Ala Gln Arg
 50           55           60
Lys Phe Gly Val Val Leu Asp Glu Ile Lys Pro Ser Ser Ala Pro Glu
 65           70           75           80
Leu Gln Ala Val Arg Met Phe Ala Asp Tyr Leu Ala His Glu Ser Arg
 85           90           95
Arg Asp Ser Ile Val Ala Glu Leu Asp Arg Glu Met Ser Arg Ser Val
100           105           110
Asp Val Thr Asn Thr Thr Phe Leu Leu Met Ala Ala Ser Ile Tyr Leu
115           120           125
His Asp Gln Asn Pro Asp Ala Ala Leu Arg Ala Leu His Gln Gly Asp
130           135           140
Ser Leu Glu Cys Thr Ala Met Thr Val Gln Ile Leu Leu Lys Leu Asp
145           150           155           160
Arg Leu Asp Leu Ala Arg Lys Glu Leu Lys Arg Met Gln Asp Leu Asp
165           170           175
Glu Asp Ala Thr Leu Thr Gln Leu Ala Thr Ala Trp Val Ser Leu Ala
180           185           190
Thr Gly Gly Glu Lys Leu Gln Asp Ala Tyr Tyr Ile Phe Gln Glu Met
195           200           205
Ala Asp Lys Cys Ser Pro Thr Leu Leu Leu Leu Asn Gly Gln Ala Ala
210           215           220
Cys His Met Ala Gln Gly Arg Trp Glu Ala Ala Glu Gly Leu Leu Gln
225           230           235           240
Glu Ala Leu Asp Lys Asp Ser Gly Tyr Pro Glu Thr Leu Val Asn Leu
245           250           255
Ile Val Leu Ser Gln His Leu Gly Lys Pro Pro Glu Val Thr Asn Arg
260           265           270
Tyr Leu Ser Gln Leu Lys Asp Ala His Arg Ser His Pro Phe Ile Lys
275           280           285
Glu Tyr Gln Ala Lys Glu Asn Asp Phe Asp Arg Leu Val Leu Gln Tyr
290           295           300
Ala Pro Ser Ala
305

```

<210> 19

<211> 3528

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 19

```

agccaaggac tctggagccg ccgcccgcgc tgctgcggtt catatccgga gtagacggag      60
ccgcagtaga cggatccgcg gctgcaccaa accactgccc ctccggagcct ggtagtgggc      120
cacaagcccc cagtcccaga ggcgtggtgg gtcgggcaga gtcggaagaa ctggctttct      180
agctggaaga tgcggaaggg gagcgactag gccgcttgcg tctgggcctg gcagaaggga      240

```

ccggattttc	tggcatcctt	aaatccttg	tcaaggattg	gttataatat	aaccagaaac	300
catgacggcg	gctgagaacg	tatgctacac	gttaattaac	gtgccaatgg	attcagaacc	360
accatctgaa	attagcttaa	aaaatgatct	agaaaaagga	gatgtaaagt	caaagactga	420
agctttgaag	aaagtaatca	ttatgattct	gaatggtgaa	aaacttcctg	gacttctgat	480
gaccatcatt	cgttttgtgc	tacctcttca	ggatcacact	atcaagaaat	tacttctggt	540
attttgggaa	attgttctta	aaacaactcc	agatgggaga	cttttacctg	agatgatcct	600
tgtatgtgat	gcatacagaa	aggatcttca	acatccta	gaatttattc	gaggatctac	660
tcttcgtttt	ctttgcaa	tgaaagaagc	agaattgcta	gaacctttta	tgccagctat	720
tcgtgcatgt	ttggagcatc	gacacagcta	tgttagaaga	aatgctgttt	tggccatcta	780
taccatctat	agaaattttg	aacatcttat	acctgatgct	cctgaactga	tacatgattt	840
tctggtgaat	gagaaggatg	caagttgcaa	aaggaatgca	tttatgatgc	taattcatgc	900
agatcaggat	cgagcttttg	attacttaag	tacttgcat	gatcaagttc	aaacatttgg	960
agacattctg	cagctgggta	ttgttgaact	gatttataag	gtctgtcatg	ctaataccatc	1020
agaaagagct	cgtttttattc	gctgcatcta	taacttatta	cagtcatcca	gccctgctgt	1080
aaaatatgaa	gctgctggga	cattagtgc	actctctagt	gcaccaactg	caatcaaggc	1140
tgctgctcag	tgttacattg	atttaattat	taaggagagc	gacaacaatg	taaaactcat	1200
agttttggat	cgtttgatag	aattaaaaga	gcacctgct	catgaacgag	tactacagga	1260
tctggttatg	gatataccta	gagtattgag	cacaccagac	ttagaagtac	gaaagaaaac	1320
tctgcagtta	gcactggatc	ttgtctcttc	tagaaatggt	gaagagctgg	ttattgtcct	1380
gaagaaggaa	gtgataaaaa	caaataatgt	gtctgagcat	gaagatactg	acaataacag	1440
acaactccta	gtgcgaacat	tgcatctctg	ttctgtccga	ttccagata	tggctgcaaa	1500
tgttattcct	tggtttaatgg	aatttctcag	tgacaacaac	gaagcagcag	ctgctgatgt	1560
cttggagttt	gttcgtgaag	ccattcagcg	ctttgataac	ctgagaatgc	ttattgttga	1620
gaagatgctt	gaagtctttc	atgctattaa	atctgtcaag	atttaccgag	gagcattatg	1680
gatcctggga	gaatactgta	gtaccaagga	agacattcag	agtgtgatga	ctgagatccg	1740
caggctccct	ggagagatcc	caattgtaga	gtcagaaata	aagaaagaag	ctgggtgaatt	1800
aaaacctgaa	gaagaaataa	ctgtagggcc	agttcagaaa	ttggttactg	aaatgggtac	1860
ctatgcaact	cagagtgc	ttagcagttc	tagaccacc	aagaaagagg	aagacagacc	1920
tcccttgaga	ggattccttc	tggatggaga	tttctttggt	gctgcctccc	ttgccacaac	1980
tctgaccaag	attgcattgc	gctatgtagc	tttggttcag	gagaagaaaa	agcaaatctc	2040
ttttgttgct	gaggctatgt	tgctcatggc	tactatcctg	catttgggaa	aatcctctct	2100
tcctaagaag	ccaattactg	atgatgatgt	ggatcgaatt	tccctgtgcc	tcaaggctct	2160
gtctgaatgt	tcacctttta	tgaatgacat	tttcaataag	gaatgcagac	agtccctttc	2220
tcacatgtta	tctgctaaac	tagaagaaga	gaaattatcc	caaaagaaag	aatctgaaaa	2280
gaggaatgtg	acagtacagc	ctgatgaccc	catttccttc	atgcaactaa	ctgctaagaa	2340
tgaaatgaac	tgcaaggaag	atcagtttca	gctgagttta	ctggcagcaa	tgggtaaacac	2400
acagaggaaa	gaggcagcag	atcccctagc	atctaaactt	aacaaggtea	cccaattgac	2460
aggtttctca	gatcctgtat	atgcagaagc	ttacgttcat	gtcaaccaat	atgatattgt	2520
cctggatgta	cttgttgtga	accaaaccag	tgatactttg	cagaattgca	cattagaact	2580
agctacacta	ggggatctga	aacttgttga	aaagccgtct	cctttgactc	ttgtcctca	2640
tgacttcgca	aatattaaag	ctaactgcaa	agtagcatca	acagaaaatg	gaataatttt	2700
tggtaataata	gtttatgatg	tctctggagc	agcaagtgc	agaaattgtg	tggttctcag	2760
tgatattcac	atcgacatca	tggactatat	ccagcctgca	acttgcaactg	atgcagaatt	2820
ccgtcagatg	tgggcccgaat	ttgaatggga	aaacaaagtg	acagttaaca	ccaacatggt	2880
tgattttaat	gactacttac	agcacatatt	aaagtcaacc	aatatgaaat	gcctgactcc	2940
agaaaaggcc	ctttctggtt	actgtggctt	tatggcagcc	aacctttatg	ctcgttccat	3000
atlttggtgaa	gatgcacttg	caaatgtcag	cattgagaag	ccaattcacc	agggaccaga	3060
tgctgctggt	accggccata	taagaattcg	tgcaagagc	cagggaatgg	ccttaagtct	3120
tggagataaaa	atcaacttgt	cacagaagaa	aactagtata	taaaaataaa	caaaaagtcc	3180
ttgaagcttt	acagttaatt	taggtatggg	cttactggac	tccaacatct	tttgtactct	3240
ttcatgctta	tatagaatct	gagttcatgc	tgaatacttt	tcagccaata	atttatagcc	3300
tttcccttaa	atcaagattg	agttaaata	tatagtttgt	cttttgtctt	aacagtctctg	3360
aatgctgtcc	tcaaagtata	taatgtttca	tgtaccaaga	cccttttcac	agtacaataa	3420
acagatctat	tcataaattt	ttgttatatt	ataaataaat	gattacataa	tttttagttat	3480
aaaaaaaaaa	aaaaaaaaaa	agaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		3528

<210> 20

<211> 953

<212> PRT

<213> Artificial Sequence

Ile	Lys	Ser	Val	Lys	Ile	Tyr	Arg	Gly	Ala	Leu	Trp	Ile	Leu	Gly	Glu
450						455					460				
Tyr	Cys	Ser	Thr	Lys	Glu	Asp	Ile	Gln	Ser	Val	Met	Thr	Glu	Ile	Arg
465					470					475					480
Arg	Ser	Leu	Gly	Glu	Ile	Pro	Ile	Val	Glu	Ser	Glu	Ile	Lys	Lys	Glu
				485					490					495	
Ala	Gly	Glu	Leu	Lys	Pro	Glu	Glu	Glu	Ile	Thr	Val	Gly	Pro	Val	Gln
			500					505					510		
Lys	Leu	Val	Thr	Glu	Met	Gly	Thr	Tyr	Ala	Thr	Gln	Ser	Ala	Leu	Ser
		515					520					525			
Ser	Ser	Arg	Pro	Thr	Lys	Lys	Glu	Glu	Asp	Arg	Pro	Pro	Leu	Arg	Gly
		530				535					540				
Phe	Leu	Leu	Asp	Gly	Asp	Phe	Phe	Val	Ala	Ala	Ser	Leu	Ala	Thr	Thr
545					550					555					560
Leu	Thr	Lys	Ile	Ala	Leu	Arg	Tyr	Val	Ala	Leu	Val	Gln	Glu	Lys	Lys
				565					570					575	
Lys	Gln	Asn	Ser	Phe	Val	Ala	Glu	Ala	Met	Leu	Leu	Met	Ala	Thr	Ile
			580					585					590		
Leu	His	Leu	Gly	Lys	Ser	Ser	Leu	Pro	Lys	Lys	Pro	Ile	Thr	Asp	Asp
		595					600					605			
Asp	Val	Asp	Arg	Ile	Ser	Leu	Cys	Leu	Lys	Val	Leu	Ser	Glu	Cys	Ser
		610				615					620				
Pro	Leu	Met	Asn	Asp	Ile	Phe	Asn	Lys	Glu	Cys	Arg	Gln	Ser	Leu	Ser
625					630					635					640
His	Met	Leu	Ser	Ala	Lys	Leu	Glu	Glu	Glu	Lys	Leu	Ser	Gln	Lys	Lys
				645					650					655	
Glu	Ser	Glu	Lys	Arg	Asn	Val	Thr	Val	Gln	Pro	Asp	Asp	Pro	Ile	Ser
			660					665					670		
Phe	Met	Gln	Leu	Thr	Ala	Lys	Asn	Glu	Met	Asn	Cys	Lys	Glu	Asp	Gln
		675					680					685			
Phe	Gln	Leu	Ser	Leu	Leu	Ala	Ala	Met	Gly	Asn	Thr	Gln	Arg	Lys	Glu
		690				695					700				
Ala	Ala	Asp	Pro	Leu	Ala	Ser	Lys	Leu	Asn	Lys	Val	Thr	Gln	Leu	Thr
705					710					715					720
Gly	Phe	Ser	Asp	Pro	Val	Tyr	Ala	Glu	Ala	Tyr	Val	His	Val	Asn	Gln
				725					730					735	
Tyr	Asp	Ile	Val	Leu	Asp	Val	Leu	Val	Val	Asn	Gln	Thr	Ser	Asp	Thr
			740					745					750		
Leu	Gln	Asn	Cys	Thr	Leu	Glu	Leu	Ala	Thr	Leu	Gly	Asp	Leu	Lys	Leu
		755					760					765			
Val	Glu	Lys	Pro	Ser	Pro	Leu	Thr	Leu	Ala	Pro	His	Asp	Phe	Ala	Asn
		770				775					780				
Ile	Lys	Ala	Asn	Val	Lys	Val	Ala	Ser	Thr	Glu	Asn	Gly	Ile	Ile	Phe
785					790					795					800
Gly	Asn	Ile	Val	Tyr	Asp	Val	Ser	Gly	Ala	Ala	Ser	Asp	Arg	Asn	Cys
				805				810						815	
Val	Val	Leu	Ser	Asp	Ile	His	Ile	Asp	Ile	Met	Asp	Tyr	Ile	Gln	Pro
			820					825					830		
Ala	Thr	Cys	Thr	Asp	Ala	Glu	Phe	Arg	Gln	Met	Trp	Ala	Glu	Phe	Glu
		835					840					845			
Trp	Glu	Asn	Lys	Val	Thr	Val	Asn	Thr	Asn	Met	Val	Asp	Leu	Asn	Asp
		850				855					860				
Tyr	Leu	Gln	His	Ile	Leu	Lys	Ser	Thr	Asn	Met	Lys	Cys	Leu	Thr	Pro
865					870					875					880
Glu	Lys	Ala	Leu	Ser	Gly	Tyr	Cys	Gly	Phe	Met	Ala	Ala	Asn	Leu	Tyr
				885					890					895	
Ala	Arg	Ser	Ile	Phe	Gly	Glu	Asp	Ala	Leu	Ala	Asn	Val	Ser	Ile	Glu
			900					905					910		
Lys	Pro	Ile	His	Gln	Gly	Pro	Asp	Ala	Ala	Val	Thr	Gly	His	Ile	Arg
			915				920					925			

ATTORNEY DOCKET 21101.0045U2

Ile Arg Ala Lys Ser Gln Gly Met Ala Leu Ser Leu Gly Asp Lys Ile
 930 935 940
 Asn Leu Ser Gln Lys Lys Thr Ser Ile
 945 950

<210> 21
 <211> 3075
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 21
 ggcactgtag caccgctact ccgtgccgcg cccgtcgagc attgcgttgc tgcattgcgc 60
 cccaccgact ccactatggt gaagaaattc gacaagaagg atgaggagtc aggtggaggc 120
 tccaacccat tccagcacct tgagaagagt gcggtactcc aggaggcccg tgtattttaat 180
 gaaactccca tcaaccctcg gaaatgtgcc cacatcctca ccaagattct ttatctcata 240
 aaccaggggg agcacctggg gaccacggaa gcgaccgagg ccttccttgc catgaccaag 300
 ctctttcagt ccaatgacct cacactccgt cggatgtgct acttgaccat caaggagatg 360
 tcttgcatgt cagaggatgt catcattgtc accagcagcc taacaaaaga catgactggg 420
 aaagaagaca actaccgggg cccggccgtg cgagccctct gccagatcac tgatagcacc 480
 atgctgcagg ctattgagcg ctacatgaaa caagccattg tggacaagggt gccagtgctc 540
 tccagctctg cctcgtgtc ttccttgcac ctgctgaagt gcagctttga cgtggtcaag 600
 cgctgggtga atgaggctca ggaggcagca tccagtata acatcatggt ccagtaccac 660
 gcaactaggg tctgtacca tgtgcgtaag aatgaccgcc tagccgtcaa taagatgac 720
 agcaaggta cacggcatgg ccttaagtct ccctttgcct actgcatgat gatccgggtg 780
 gccagcaagc agctggaaga ggaggatggc agccgtgaca gccactgtt tgacttcac 840
 gagagctgct tgcgcaacaa gcacgagatg tgggtgtatg aagccgcctc ggccattgtc 900
 aacctgcctg ggtgcagcgc caaggagctg gccccagctg tctcagtgtc ccagctcttc 960
 tgcagctccc ccaaggccgc cctccgttac gccgcgctc gcaccctcaa caagggtggc 1020
 atgaagcacc cgtccgctgt gacagcttgt aatctggatc tggagaacct ggtcacagat 1080
 tcaaacgcga gcattgccac gctggccatc accaccctcc ttaagacggg cagcgagagc 1140
 agcatcgacc gcctcatgaa gcagatctcc tcttcatgt cagaaatctc ggatgaattc 1200
 aagggtggtg ttgtccaggc catcagtgcc ctgtgtcaga aatatcctcg caaacacgcc 1260
 gtcttatga acttctgtt caccatgctg cgggaagagg gtggctttga gtataagcgc 1320
 gctatcgttg actgcatcat cagcatcatt gaagagaact cagagagcaa ggagacagg 1380
 ctgtcacatc tgtgcgagtt catcgaggac tgcgagttca cagtgtggtc caccgtatt 1440
 ctacatctcc tgggccagga ggggcccaag accaccaatc cctcaaagta catccgttc 1500
 atctataacc gagtgtgtt ggagcatgag gaggtccggg cagggtgctg gagtgtctg 1560
 gcgaagtttg gagcccagaa tgaagagatg ttaccagta tcttggtgtt gctgaagagg 1620
 tgtgtgatgg atgatgacaa tgaagtaagg gaccgagcca ccttctacct aaatgtctc 1680
 gagcagaagc agaaggccct taatgcaggc tatatcctaa atggtctgac tgtgtccatc 1740
 cctggtcttg agagggtctc gcagcagtac actctagaac catcagaaaa accttttgac 1800
 ctcaagtctg tgcccctggc cacggcgccc atggcagagc agagaacaga aagtaccccc 1860
 atcacagcag tcaaacagcc tgagaaagtg gcagctacca ggcaggagat cttccaggag 1920
 cagttggcag cagtgccaga gttccgcggt cttgggcccc tcttcaagtc ctgcctgag 1980
 cccgtggccc tcaccgagtc agagacggag tatgtcatcc gctgcaccaa acacaccttc 2040
 accaaccaca tgggtttttca gtttgactgc acaaacacac tcaatgacca gacctggag 2100
 aatgtcacag tgcagatgga gccactgag gcctatgagg tgctctgtta cgtgcctgcc 2160
 cggagcctgc cctacaacca gcccgggacc tgctacacac tgggtggcact gcccaaagaa 2220
 gacccacag ctgtggcctg cacattcagc tgcagatga agttcactgt caaggactgt 2280
 gatccacca ctggggagac tgatgacgaa ggctatgagg atgagtatgt gctggaagat 2340
 ctggaagtta ctgtagctga tcacattcaa aaggtcatga aactgaactc cgaagcagcc 2400
 tgggatgagg taggggatga atttgagaag gaggaacgt tcacctgtc taccatcaag 2460
 acactgaag aggtgtgtgg taatattgtg aagttcttgg gaatgcaccc ttgtgagagg 2520
 tcagacaaag tgccggataa caagaacacc cacacgttgc tctgggtgg tgtgttccgg 2580
 ggtggtcatg acatcctggt gcgctcccgg ctgctgcttt tggacacagt gacaatgcag 2640
 gtgacagcca gaagtttggg ggagctgcca gtagacatca tcttggcatc tgtgggataa 2700
 gaggccagcc tgcataaggac ctcataccct tccccaacac tacctggaag ttgtgccttc 2760

```

ctcatgaaac tggcagaaac cccttcccaa gcttctgtat tgaaaaacaa ttaggaatca 2820
ttgcagattt ttttttattc tgctccacc tcccaccgg gactacttgc tggtgacttt 2880
tttttttttt ttttttaaatt aggggatgat tttagcttgt cctaaatctt gctgtccacc 2940
cttccaggaa agggacattg taaatgaata aaacattctc aactcctctt gaatctatcc 3000
cccaagaaac catcttatcc ctgtaataaa tcagcatgta tttattgaaa aaaaaaaaaa 3060
aaaaaaaaaa aaaaaa 3075

```

<210> 22

<211> 874

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 22

```

Met Leu Lys Lys Phe Asp Lys Lys Asp Glu Glu Ser Gly Gly Gly Ser
 1          5          10          15
Asn Pro Phe Gln His Leu Glu Lys Ser Ala Val Leu Gln Glu Ala Arg
 20          25          30
Val Phe Asn Glu Thr Pro Ile Asn Pro Arg Lys Cys Ala His Ile Leu
 35          40          45
Thr Lys Ile Leu Tyr Leu Ile Asn Gln Gly Glu His Leu Gly Thr Thr
 50          55          60
Glu Ala Thr Glu Ala Phe Phe Ala Met Thr Lys Leu Phe Gln Ser Asn
 65          70          75          80
Asp Pro Thr Leu Arg Arg Met Cys Tyr Leu Thr Ile Lys Glu Met Ser
 85          90          95
Cys Ile Ala Glu Asp Val Ile Ile Val Thr Ser Ser Leu Thr Lys Asp
100          105          110
Met Thr Gly Lys Glu Asp Asn Tyr Arg Gly Pro Ala Val Arg Ala Leu
115          120          125
Cys Gln Ile Thr Asp Ser Thr Met Leu Gln Ala Ile Glu Arg Tyr Met
130          135          140
Lys Gln Ala Ile Val Asp Lys Val Pro Ser Val Ser Ser Ser Ala Leu
145          150          155          160
Val Ser Ser Leu His Leu Leu Lys Cys Ser Phe Asp Val Val Lys Arg
165          170          175
Trp Val Asn Glu Ala Gln Glu Ala Ala Ser Ser Asp Asn Ile Met Val
180          185          190
Gln Tyr His Ala Leu Gly Leu Leu Tyr His Val Arg Lys Asn Asp Arg
195          200          205
Leu Ala Val Asn Lys Met Ile Ser Lys Val Thr Arg His Gly Leu Lys
210          215          220
Ser Pro Phe Ala Tyr Cys Met Met Ile Arg Val Ala Ser Lys Gln Leu
225          230          235          240
Glu Glu Glu Asp Gly Ser Arg Asp Ser Pro Leu Phe Asp Phe Ile Glu
245          250          255
Ser Cys Leu Arg Asn Lys His Glu Met Val Val Tyr Glu Ala Ala Ser
260          265          270
Ala Ile Val Asn Leu Pro Gly Cys Ser Ala Lys Glu Leu Ala Pro Ala
275          280          285
Val Ser Val Leu Gln Leu Phe Cys Ser Ser Pro Lys Ala Ala Leu Arg
290          295          300
Tyr Ala Ala Val Arg Thr Leu Asn Lys Val Ala Met Lys His Pro Ser
305          310          315          320
Ala Val Thr Ala Cys Asn Leu Asp Leu Glu Asn Leu Val Thr Asp Ser
325          330          335
Asn Arg Ser Ile Ala Thr Leu Ala Ile Thr Thr Leu Leu Lys Thr Gly
340          345          350

```

Ser	Glu	Ser	Ser	Ile	Asp	Arg	Leu	Met	Lys	Gln	Ile	Ser	Ser	Phe	Met
		355					360					365			
Ser	Glu	Ile	Ser	Asp	Glu	Phe	Lys	Val	Val	Val	Val	Gln	Ala	Ile	Ser
		370					375					380			
Ala	Leu	Cys	Gln	Lys	Tyr	Pro	Arg	Lys	His	Ala	Val	Leu	Met	Asn	Phe
385					390					395					400
Leu	Phe	Thr	Met	Leu	Arg	Glu	Glu	Gly	Gly	Phe	Glu	Tyr	Lys	Arg	Ala
				405					410						415
Ile	Val	Asp	Cys	Ile	Ile	Ser	Ile	Ile	Glu	Glu	Asn	Ser	Glu	Ser	Lys
			420					425					430		
Glu	Thr	Gly	Leu	Ser	His	Leu	Cys	Glu	Phe	Ile	Glu	Asp	Cys	Glu	Phe
		435					440					445			
Thr	Val	Leu	Ala	Thr	Arg	Ile	Leu	His	Leu	Leu	Gly	Gln	Glu	Gly	Pro
		450				455					460				
Lys	Thr	Thr	Asn	Pro	Ser	Lys	Tyr	Ile	Arg	Phe	Ile	Tyr	Asn	Arg	Val
465					470					475					480
Val	Leu	Glu	His	Glu	Glu	Val	Arg	Ala	Gly	Ala	Val	Ser	Ala	Leu	Ala
				485					490						495
Lys	Phe	Gly	Ala	Gln	Asn	Glu	Glu	Met	Leu	Pro	Ser	Ile	Leu	Val	Leu
			500					505				510			
Leu	Lys	Arg	Cys	Val	Met	Asp	Asp	Asp	Asn	Glu	Val	Arg	Asp	Arg	Ala
		515					520					525			
Thr	Phe	Tyr	Leu	Asn	Val	Leu	Glu	Gln	Lys	Gln	Lys	Ala	Leu	Asn	Ala
		530				535					540				
Gly	Tyr	Ile	Leu	Asn	Gly	Leu	Thr	Val	Ser	Ile	Pro	Gly	Leu	Glu	Arg
545					550					555					560
Ala	Leu	Gln	Gln	Tyr	Thr	Leu	Glu	Pro	Ser	Glu	Lys	Pro	Phe	Asp	Leu
				565					570					575	
Lys	Ser	Val	Pro	Leu	Ala	Thr	Ala	Pro	Met	Ala	Glu	Gln	Arg	Thr	Glu
			580					585					590		
Ser	Thr	Pro	Ile	Thr	Ala	Val	Lys	Gln	Pro	Glu	Lys	Val	Ala	Ala	Thr
		595					600					605			
Arg	Gln	Glu	Ile	Phe	Gln	Glu	Gln	Leu	Ala	Ala	Val	Pro	Glu	Phe	Arg
		610				615					620				
Gly	Leu	Gly	Pro	Leu	Phe	Lys	Ser	Ser	Pro	Glu	Pro	Val	Ala	Leu	Thr
625					630					635					640
Glu	Ser	Glu	Thr	Glu	Tyr	Val	Ile	Arg	Cys	Thr	Lys	His	Thr	Phe	Thr
				645					650					655	
Asn	His	Met	Val	Phe	Gln	Phe	Asp	Cys	Thr	Asn	Thr	Leu	Asn	Asp	Gln
			660				665					670			
Thr	Leu	Glu	Asn	Val	Thr	Val	Gln	Met	Glu	Pro	Thr	Glu	Ala	Tyr	Glu
		675					680					685			
Val	Leu	Cys	Tyr	Val	Pro	Ala	Arg	Ser	Leu	Pro	Tyr	Asn	Gln	Pro	Gly
		690				695					700				
Thr	Cys	Tyr	Thr	Leu											

Val Phe Arg Gly Gly His Asp Ile Leu Val Arg Ser Arg Leu Leu Leu
 835 840 845
 Leu Asp Thr Val Thr Met Gln Val Thr Ala Arg Ser Leu Glu Glu Leu
 850 855 860
 Pro Val Asp Ile Ile Leu Ala Ser Val Gly
 865 870

<210> 23
 <211> 3110
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 23
 tcgccggctg cggcgccctg gacgggttgcg gtgggtctg ggcgtgggaa gtcgtccaag 60
 atgattaaaa aattcgacaa gaaggacgag gagtctggta gtggctccaa tcctttccag 120
 catctggaga agagtgtgt tttacaggag gctcgtatat tcaatgaaac tccaatcaat 180
 ccaagaagat gtttgcata tcttaccaaag attctttact tactgaacca ggggtgaacac 240
 tttggaacaa cggaagctac agaagccttc tttgcaatga cgcgattgtt tcaatctaata 300
 gatcaaacat tgaggagaat gtgctacctt accatcaaag aaatggctac catctctgag 360
 gatgtgataa ttgtcacaag cagtctgact aaagacatga ctggaaaaga agatgtatac 420
 cgaggcccg ccatcagagc tctctgcagg atcaccgatg gaacaatgtt gcaagccatt 480
 gaaagataca tgaagcaggc cattgtggat aaagtttcca gtgtatccag ttcagcactg 540
 gtatcttccc tgcacatgat gaagataagc tatgatgtgg ttaagcgctg gatcaatgaa 600
 gcccagaag ctgcatcaag tgataatatt atggtccagt accatgcatt gggagtcctg 660
 tatcacctta gaaagaatga tcgacttgct gtttccaaga tgttgataaa gtttactaaa 720
 tctgggtctca agtcacagtt tgcttactgc atgctgatcc gaattgccag tcgcttacta 780
 aaagaaactg aggatggcca tgaaagtcca ctgtttgatt tcattgagag ctgcttgcca 840
 aataaacatg aaatgggtat ttatgaagct gcttcagcta tcatccatct tcctaactgc 900
 actgcaagag agttggcacc tgctgtttca gttcttcaac ttttctgtag ttctcctaag 960
 ccagccttga gatatgcagc tgtgaggacc ttgaacaagg tggcaatgaa gcacccctct 1020
 gctgttactg cctgcaatct ggacttagaa aacttaatac cagactcaaa cagaagcatt 1080
 gctaccttag ccattactac actcctcaaa acaggaagtg agagcagtgt ggaccggctc 1140
 atgaagcaga tatcttcttt tgtgtctgaa atctcagatg agttcaaggt ggtggttgta 1200
 caggcaatta gtgctctctg tcagaaatac cctcgaaagc acagtgtcat gatgactttc 1260
 ctctccaaca tgctccgaga tgatggaggc tttgagtaca agcgggccat tgtggactgt 1320
 ataatacaga ttgtggaaga gaacctgag agtaagaag caggcctagc ccaccttgt 1380
 gaattcattg aggactgtga acacactgtt ctggctacta agattctaca cttgttgggc 1440
 aaagagggcc ctagaacgcc tgtccctccc aaatatatcc gttttatatt taatagggtt 1500
 gtccctggaga atgaggtgt cagagctgct gctgtgagtg ctttggctaa atttggggct 1560
 cagaatgaga gtcttctccc aagcatcctt gtactcttac agagggtgat gatggatact 1620
 gatgacgagg tacgagacag agctaccttc tatctgaatg tgctgcagca gaggcagatg 1680
 gcactaaatg ccacatata cttaaatggt ttgacggctc ctgtaccagg gatggaaaaa 1740
 gccttacacc agtacacgtt ggagccttca gaaaaaccgt ttgacatgaa atcaattcct 1800
 cttgctatgg ctctgtctt tgaacagaaa gcagaaatca cacttgtggc tactaagcca 1860
 gagaagttgg ctcttccag gcaagacatt ttccaagaac aattggctgc cattcctgag 1920
 tttctgaata taggacctt gttcaagtct tctgagcctg ttcaacttac agaagcagag 1980
 acagaatatt ttgttcgatg tatcaagcac atgtttacca atcacatcgt gttccagttt 2040
 gactgcacca acactctcaa tgaccagctg ctggaaaaag tgacagtgc gatggagcca 2100
 tcagattcct atgaagtgt gtcttgatc ccagccccc gccttcctta taaccaacca 2160
 ggaatatgtt acactcttgt tcgtttgcct gatgatgacc ctacagcagt tgcaggctcc 2220
 tttagtgcga ccatgaagtt tacagtccgg gactgtgacc ctaacactgg agttccagat 2280
 gaggatgggt atgatgtga gtatgtgct gaagatctcg aagtgactgt gtctgacct 2340
 attcagaaag tactgaagcc taactttgtc gctgcttggg aagagggtgg agatacctt 2400
 gagaaagagg aaacctttgc cctcagttct accaaaacc ttgaagaggc tgtcaacaat 2460
 atcatcacat ttctgggcat gcagccatgt gagaggctcg ataaagtacc tgagaacaag 2520
 aattcccatt cgctctatct ggaggtata ttcagagggt gctatgattt attggtgagg 2580
 tccaggctgg ccttagccga tggagtgacc atgcagggtga ctgtcagaag taaagagaga 2640

```

acacctgtag atgttatctt agcttctgtt ggataaatgc ttactggaca agaggaaact 2700
gatgcacact acatggtcag tgggctttta ggctagtggc atcagtttcc cagaatcaga 2760
cttttgaaga tgaatgactt tggagaagca aattaaacat ttggccctga gccagcagat 2820
caagcaaatg tctatctttg cgcattgggtt gttttttttt tttttctttt tattctactt 2880
ggtcagcttt gggacgatag tgcagctttg ggtgatcttg aaaatcaaact actatcctat 2940
actccagctg cttaacttca ttttattctt taatgtgtac ctgaaagctc ctgggcaatgc 3000
tggaaaattt ttatcccaga ggggtggggg ggagggggga ggggaagcca gagtccactt 3060
ttgtcacaaat tcattttttat taatagaaaa taaacactta ttccagtttc 3110

```

<210> 24

<211> 871

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 24

```

Met Ile Lys Lys Phe Asp Lys Lys Asp Glu Glu Ser Gly Ser Gly Ser
1          5          10          15
Asn Pro Phe Gln His Leu Glu Lys Ser Ala Val Leu Gln Glu Ala Arg
20          25          30
Ile Phe Asn Glu Thr Pro Ile Asn Pro Arg Arg Cys Leu His Ile Leu
35          40          45
Thr Lys Ile Leu Tyr Leu Leu Asn Gln Gly Glu His Phe Gly Thr Thr
50          55          60
Glu Ala Thr Glu Ala Phe Phe Ala Met Thr Arg Leu Phe Gln Ser Asn
65          70          75          80
Asp Gln Thr Leu Arg Arg Met Cys Tyr Leu Thr Ile Lys Glu Met Ala
85          90          95
Thr Ile Ser Glu Asp Val Ile Ile Val Thr Ser Ser Leu Thr Lys Asp
100         105         110
Met Thr Gly Lys Glu Asp Val Tyr Arg Gly Pro Ala Ile Arg Ala Leu
115         120         125
Cys Arg Ile Thr Asp Gly Thr Met Leu Gln Ala Ile Glu Arg Tyr Met
130         135         140
Lys Gln Ala Ile Val Asp Lys Val Ser Ser Val Ser Ser Ala Leu
145         150         155         160
Val Ser Ser Leu His Met Met Lys Ile Ser Tyr Asp Val Val Lys Arg
165         170         175
Trp Ile Asn Glu Ala Gln Glu Ala Ala Ser Ser Asp Asn Ile Met Val
180         185         190
Gln Tyr His Ala Leu Gly Val Leu Tyr His Leu Arg Lys Asn Asp Arg
195         200         205
Leu Ala Val Ser Lys Met Leu Asn Lys Phe Thr Lys Ser Gly Leu Lys
210         215         220
Ser Gln Phe Ala Tyr Cys Met Leu Ile Arg Ile Ala Ser Arg Leu Leu
225         230         235         240
Lys Glu Thr Glu Asp Gly His Glu Ser Pro Leu Phe Asp Phe Ile Glu
245         250         255
Ser Cys Leu Arg Asn Lys His Glu Met Val Ile Tyr Glu Ala Ala Ser
260         265         270
Ala Ile Ile His Leu Pro Asn Cys Thr Ala Arg Glu Leu Ala Pro Ala
275         280         285
Val Ser Val Leu Gln Leu Phe Cys Ser Ser Pro Lys Pro Ala Leu Arg
290         295         300
Tyr Ala Ala Val Arg Thr Leu Asn Lys Val Ala Met Lys His Pro Ser
305         310         315         320
Ala Val Thr Ala Cys Asn Leu Asp Leu Glu Asn Leu Ile Thr Asp Ser
325         330         335

```

Asn	Arg	Ser	Ile	Ala	Thr	Leu	Ala	Ile	Thr	Thr	Leu	Leu	Lys	Thr	Gly	340	345	350
Ser	Glu	Ser	Ser	Val	Asp	Arg	Leu	Met	Lys	Gln	Ile	Ser	Ser	Phe	Val	355	360	365
Ser	Glu	Ile	Ser	Asp	Glu	Phe	Lys	Val	Val	Val	Val	Gln	Ala	Ile	Ser	370	375	380
Ala	Leu	Cys	Gln	Lys	Tyr	Pro	Arg	Lys	His	Ser	Val	Met	Met	Thr	Phe	385	390	395
Leu	Ser	Asn	Met	Leu	Arg	Asp	Asp	Gly	Gly	Phe	Glu	Tyr	Lys	Arg	Ala	405	410	415
Ile	Val	Asp	Cys	Ile	Ile	Ser	Ile	Val	Glu	Glu	Asn	Pro	Glu	Ser	Lys	420	425	430
Glu	Ala	Gly	Leu	Ala	His	Leu	Cys	Glu	Phe	Ile	Glu	Asp	Cys	Glu	His	435	440	445
Thr	Val	Leu	Ala	Thr	Lys	Ile	Leu	His	Leu	Leu	Gly	Lys	Glu	Gly	Pro	450	455	460
Arg	Thr	Pro	Val	Pro	Ser	Lys	Tyr	Ile	Arg	Phe	Ile	Phe	Asn	Arg	Val	465	470	475
Val	Leu	Glu	Asn	Glu	Ala	Val	Arg	Ala	Ala	Ala	Val	Ser	Ala	Leu	Ala	485	490	495
Lys	Phe	Gly	Ala	Gln	Asn	Glu	Ser	Leu	Leu	Pro	Ser	Ile	Leu	Val	Leu	500	505	510
Leu	Gln	Arg	Cys	Met	Met	Asp	Thr	Asp	Asp	Glu	Val	Arg	Asp	Arg	Ala	515	520	525
Thr	Phe	Tyr	Leu	Asn	Val	Leu	Gln	Gln	Arg	Gln	Met	Ala	Leu	Asn	Ala	530	535	540
Thr	Tyr	Ile	Phe	Asn	Gly	Leu	Thr	Val	Ser	Val	Pro	Gly	Met	Glu	Lys	545	550	555
Ala	Leu	His	Gln	Tyr	Thr	Leu	Glu	Pro	Ser	Glu	Lys	Pro	Phe	Asp	Met	565	570	575
Lys	Ser	Ile	Pro	Leu	Ala	Met	Ala	Pro	Val	Phe	Glu	Gln	Lys	Ala	Glu	580	585	590
Ile	Thr	Leu	Val	Ala	Thr	Lys	Pro	Glu	Lys	Leu	Ala	Pro	Ser	Arg	Gln	595	600	605
Asp	Ile	Phe	Gln	Glu	Gln	Leu	Ala	Ala	Ile	Pro	Glu	Phe	Leu	Asn	Ile	610	615	620
Gly	Pro	Leu	Phe	Lys	Ser	Ser	Glu	Pro	Val	Gln	Leu	Thr	Glu	Ala	Glu	625	630	635
Thr	Glu	Tyr	Phe	Val	Arg	Cys	Ile	Lys	His	Met	Phe	Thr	Asn	His	Ile	645	650	655
Val	Phe	Gln	Phe	Asp	Cys	Thr	Asn	Thr	Leu	Asn	Asp	Gln	Leu	Leu	Glu	660	665	670
Lys	Val	Thr	Val	Gln	Met	Glu	Pro	Ser	Asp	Ser	Tyr	Glu	Val	Leu	Ser	675	680	685
Cys	Ile	Pro	Ala	Pro	Ser	Leu	Pro	Tyr	Asn	Gln	Pro	Gly	Ile	Cys	Tyr	690	695	700
Thr	Leu	Val	Arg	Leu	Pro	Asp	Asp	Asp	Pro	Thr	Ala	Val	Ala	Gly	Ser	705	710	715
Phe	Ser	Cys	Thr	Met	Lys	Phe	Thr	Val	Arg	Asp	Cys	Asp	Pro	Asn	Thr	725	730	735
Gly	Val	Pro	Asp	Glu	Asp	Gly	Tyr	Asp	Asp	Glu	Tyr	Val	Leu	Glu	Asp	740	745	750
Leu	Glu	Val	Thr	Val	Ser	Asp	His	Ile	Gln	Lys	Val	Leu	Lys	Pro	Asn	755	760	765
Phe	Ala	Ala	Ala	Trp	Glu	Glu	Val	Gly	Asp	Thr	Phe	Glu	Lys	Glu	Glu	770	775	780
Thr	Phe	Ala	Leu	Ser	Ser	Thr	Lys	Thr	Leu	Glu	Glu	Ala	Val	Asn	Asn	785	790	795
Ile	Ile	Thr	Phe	Leu	Gly	Met	Gln	Pro	Cys	Glu	Arg	Ser	Asp	Lys	Val	805	810	815

ATTORNEY DOCKET 21101.0045U2

Pro Glu Asn Lys Asn Ser His Ser Leu Tyr Leu Ala Gly Ile Phe Arg
 820 825 830
 Gly Gly Tyr Asp Leu Leu Val Arg Ser Arg Leu Ala Leu Ala Asp Gly
 835 840 845
 Val Thr Met Gln Val Thr Val Arg Ser Lys Glu Arg Thr Pro Val Asp
 850 855 860
 Val Ile Leu Ala Ser Val Gly
 865 870

<210> 25

<211> 1900

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 25

ttttgctggct	ccacgtcggc	accagctgcg	gggcaagatg	gaggcgctga	ttttggaacc	60
ttccctgtat	actgtcaaag	ccatcctgat	tctggacaat	gatggagatc	gactttttgc	120
caagtactat	gacgacacct	acccagtggt	caaggagcaa	aaggcctttg	agaagaacat	180
tttcaacaag	acccatcgga	ctgacagtga	aattgccctc	ttggaaggcc	tgacagtggg	240
atacaaaagc	agtatagatc	tctatttcta	tgtgattggc	agctcctatg	aaaatgagct	300
gatgcttatg	gctgttctga	actgtctctt	cgactcattg	agccagatgc	tgaggaaaaa	360
tgtagaaaag	cgagcactgc	tggagaacat	ggaggggctg	ttcttggtcg	tggatgaaat	420
tgtagatgga	ggggtgatcc	tagagagtga	tccccagcag	gtggtacacc	gggtggcatt	480
aaggggtgaa	gatgtcccc	ttacggagca	gaccgtgtct	cagggtgctgc	agtcagccaa	540
agaacagatc	aagtggctac	tccttcgggtg	aagacctcac	tgttctctggc	tcttcctcct	600
cttcaaaaaa	tttgcattgtc	tgtgtggaat	tttcatctag	ttccccaatc	gatgctctca	660
gggtcatctc	ggggatcaca	gggatcctta	aatctccatt	ctgtttgtgg	ttgccccctc	720
aacctcccc	acacccttcc	tattcttttt	cattcttctt	gcagttctgg	gagtaaagct	780
cccagcatat	ttagataata	gggcagggga	agcaccctct	ttctttctag	actggattat	840
gctcacatgc	tcccttgccc	tgacattttt	gtaaattctg	tgccctttgc	tgtagctaca	900
cttcagatta	aagtaggaga	aagaatgtgc	tgagtgtttt	cctccctttg	cctctacctg	960
gccctcatcc	caacagccca	gcaaggggag	agagaaagag	aattcttttc	tatagaacga	1020
gtgggggctg	ggatgggtag	ggatttatcc	aatctaagcc	ctaaccctac	ttagtgcct	1080
cagtgttttc	ttccattcct	tcttactgcc	ctgtcctctg	ccttggaaga	ggctttggga	1140
atagttcata	gggaaggagc	aacatggaag	aaacagcgat	ttaaattgta	ttgaacaggg	1200
catataaaat	gcattctgta	ccctgatctg	gcataatagc	tcaaaaactgc	agtggcgagt	1260
gtccatctct	tagttagcta	ccttaactgt	ccacccttac	tacctgtggg	atcgttgcct	1320
ggtttgtctt	ctctgtgtcc	tggagcaaag	ccagttccta	aaactaaaac	tccattctag	1380
tcttgggaag	aaaagtctct	actcagaact	ggggaaggag	tggaaacttat	gacttggggc	1440
tctaggtctg	ctctgtcccc	tcagctcccc	gacatgcatt	tactctctgc	cgtgggtctg	1500
cagtcgctgc	aacctaccct	ctctctgcct	cagccttaca	cccaagcagt	aggtctgtgc	1560
tctccctgtc	tctaggtcgc	tgagagaggt	gcttttcttc	ataaaacctt	tggggtttgg	1620
atttccccag	gaagatggag	aatggaatac	tcactcttgg	gtctaactct	tccccttgac	1680
ccagaacttc	ctccccacaa	aaatgccttt	aaaaaccttc	ctgagactta	agcattctgc	1740
cccacttact	aactgccagt	tctccagcac	tgaggtgggg	cagataacgg	ggcatattta	1800
agggggcatc	tttgtgtaaa	agatgcatgg	agtcaggaga	aaaccacctt	cataaactgc	1860
tctgtgcaaa	gaggaataaa	acattttttc	caaactgaaa			1900

<210> 26

<211> 177

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 26

Met Glu Ala Leu Ile Leu Glu Pro Ser Leu Tyr Thr Val Lys Ala Ile
 1 5 10 15
 Leu Ile Leu Asp Asn Asp Gly Asp Arg Leu Phe Ala Lys Tyr Tyr Asp
 20 25 30
 Asp Thr Tyr Pro Ser Val Lys Glu Gln Lys Ala Phe Glu Lys Asn Ile
 35 40 45
 Phe Asn Lys Thr His Arg Thr Asp Ser Glu Ile Ala Leu Leu Glu Gly
 50 55 60
 Leu Thr Val Val Tyr Lys Ser Ser Ile Asp Leu Tyr Phe Tyr Val Ile
 65 70 75 80
 Gly Ser Ser Tyr Glu Asn Glu Leu Met Leu Met Ala Val Leu Asn Cys
 85 90 95
 Leu Phe Asp Ser Leu Ser Gln Met Leu Arg Lys Asn Val Glu Lys Arg
 100 105 110
 Ala Leu Leu Glu Asn Met Glu Gly Leu Phe Leu Ala Val Asp Glu Ile
 115 120 125
 Val Asp Gly Gly Val Ile Leu Glu Ser Asp Pro Gln Gln Val Val His
 130 135 140
 Arg Val Ala Leu Arg Gly Glu Asp Val Pro Leu Thr Glu Gln Thr Val
 145 150 155 160
 Ser Gln Val Leu Gln Ser Ala Lys Glu Gln Ile Lys Trp Ser Leu Leu
 165 170 175
 Arg

<210> 27

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 27

Cys Glu Ser Gly Glu Leu Lys Pro Glu Asp Asp Val Thr Val Gly Pro
 1 5 10 15
 Ala Gln Lys

<210> 28

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 28

Gly Asn Met Phe Ala Asn Leu Phe Lys Gly Leu Phe Gly Lys Lys Glu
 1 5 10 15

<210> 29

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =

synthetic construct

<400> 29

Glu Lys Lys Gly Phe Leu Gly Lys Phe Leu Asn Ala Phe Met Asn Gly
 1 5 10 15

<210> 30

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 30

Cys Thr His Pro Phe Thr His Glu Cys Gly Gly Gly Ser
 1 5 10

<210> 31

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 31

Cys Gly Glu His Val Arg Pro Ser Cys Gly Gly Gly Ser
 1 5 10

<210> 32

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 32

Cys Asn Asn Thr Arg Ser Pro Tyr Cys Gly Gly Gly Ser
 1 5 10

<210> 33

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 33

Cys Glu Gln Thr Leu Tyr Arg Val Cys Gly Gly Gly Ser
 1 5 10

<210> 34
 <211> 3916
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 34
 gcttgggggccc gccatctcttg caagaggcgga agcggcgagcg gttcctgtca aggggggcagc 60
 aggtccagag ctgctggtgc tcccgttccc cagaccctac cccatccccc agtggagccg 120
 gagtgcgggc gcgccccacc accgcctca ccatggtgct gttggcagca gcggtctgca 180
 caaaagcagg aaaggtatt gtttctcgac agtttgtgga aatgaccgga actcggattg 240
 agggcttatt agcagctttt ccaaagctca tgaacactgg aaaacaacat acgtttgttg 300
 aaacagagag tgaagatat gtctaccagc ctatggagaa actgtatatg gtactgatca 360
 ctacaaaaaa cagcaacatt ttagaagatt tggagaccct aaggctcttc tcaagagtga 420
 tccctgaata ttgccgagcc ttagaagaga atgaaatata tgagcactgt tttgatttga 480
 tttttgcttt tgatgaaatt gtcgcactgg gataccggga gaatgttaac ttggcacaga 540
 tcagaacctt cacagaaatg gattctcatg aggagaaggt gttcagagcc gtcagagaga 600
 ctcaagaacg tgaagctaag gctgagatgc gtcgtaaagc aaaggaatta caacaggccc 660
 gaagagatgc agagagacag ggcaaaaaag caccaggatt tggcggattt ggcagctctg 720
 cagtatctgg aggcagcaca gctgccatga tcacagagac catcattgaa actgataaac 780
 caaaagtggc acctgcacca gccaggcctt caggccccag caaggcttta aaacttggag 840
 ccaaaggaaa ggaagtagat aactttgtgg acaaattaaa atctgaaggt gaaaccatca 900
 tgtcctctag tatgggcaag cgtacttctg aagcaaccaa aatgcatgct ccaccatta 960
 atatggaaaag tgtacatatg aagattgaag aaaagataac attaacctgt ggacgagacg 1020
 gaggattaca gaatatggag ttgcatggca tgatcatgct taggatctca gatgacaagt 1080
 atggccgaat tcgtcttcat gtggaaaatg aagataagaa aggggtgcag ctacagacc 1140
 atccaaatgt ggcataaaaa ctttctactg cagagctctc aattggcctg aagaatccag 1200
 agaagtcatt tccagtcaac agtgacgtag ggggtgctaaa gtggagacta caaaccacag 1260
 aggaatcttt tattccactg acaatttaatt gctggccctc ggagagtggga aatggctgtg 1320
 atgtcaacat agaatatgag ctacaagaag ataatttaga actgaatgat gtggttatca 1380
 ccatccact cccgtctggt gtcggcgcg cgtttatcgg tgagatcgat ggggagatc 1440
 gacatgacag tcgacgaaat accctggagt ggtgcctgcc tgtgattgat gccaaaaata 1500
 agagtggcag cctggagttt agcattgctg ggcagcccaa tgacttcttc cctgttcaag 1560
 tttcctttgt ctccaagaaa aattactgta acatacaggt taccaaagtg acccaggtag 1620
 atggaaacag ccccgctcagg ttttccacag agaccacttt cctagtggat aagatgaaa 1680
 ttctgtaata ccaagaagag ggagctgaaa aggaaaattt tcagattaat aaagaagacg 1740
 ccaatgatgg ctgaagagtt tttccagat ttacaagcca ctggagaccc ctttttctg 1800
 atacaatgca cgattctctg cgcgcaagga ccctcgactc acccccatgt ttcagtgtca 1860
 cagagacatt ctttgataag gaaatggcac aaacataaag ggaaaggctg ctaattttct 1920
 ttggcagatt gtattggcca gcaggaaagc aagctctcca gagaatgccc ccagttaaat 1980
 acctcctcta cctttacctt agttgctcct ttatttttat ttattattat 2040
 tattattttt tgagatggag tctcactttg taaccagggc tggaatgcaa tggcatgatc 2100
 tcagctcact gcaacctccg cctcctgggt tcaagcaagt ctctgcctc agcctccgag 2160
 tagctgggac tacaggtgca cgccaccag cctggctaatt ttttgtatt ttagtagaga 2220
 cggggtttca ccgtgttgcc caggctggtc gcgaactcct gagctcaggc aatccgcca 2280
 cctcagcctc ccaaagtgtt gggattacag gcatgagcca ccatgccag ctgctccttt 2340
 attttaatcc cttaaataaa tccctaaata tagttatatt tcatacttag tttgttttta 2400
 aaaagttttc tctgtagaaa attttaatca ttcataacct ttaccttag gtttttcttt 2460
 ctatacatte agtcaggcac tgggatcatc tgtttacagg cattatattt atttggcact 2520
 cctggaacaa gtatatctaa ccattcttg atttttggac tattcagggtg aactatttga 2580
 ggggtatggg gtctagaagt taaaagatac gcatgtcttc tgttcttttc ccgtatcaat 2640
 tcattccttc atctctttgc caagtgttt tcttttcagg gcctgtcctt ccagtttaga 2700
 acagtacct gaatcccat tgtgtcaata ttaaagatag ctgagaagca cttttcaat 2760
 ggcacagtc cctctcaaga tgtctaaaag aatggttatg tctgtccagt tagggatttc 2820
 acatccacat gtaatcatgt ctgctgctgt tgctacccaa attttcattt ctccacattt 2880
 tgggtactta agctaaaacg taatggccac agtctgtaat ccattcacat tctcagttt 2940
 caccacctcc ctctccaga ctgcactctc tgtcatcagt cccctccttt ctaacagaaa 3000
 tggggttatg attttgaagg ctgtgggttc agggagtctt tgccaatcct gttggcccta 3060

```

aactatcaag gaggtcccat ttcaccattt gatttttttgc atttcaggag gcaactgatt 3120
gtttcgatat gtacatatta ctacagtata cccattttcc ttccagtcag cccaacattt 3180
tccaccagtc tgtcccatc tctgaaatcc ttctttctct tttcccttaa gtcttttgag 3240
tgtcatcatg tactgggtgt ttctcggttc catctcatcc atttcctttt caatggagac 3300
tacagcgtca gccagctcag ccttggcttt taactcaata ttccagtcca taggggtggt 3360
taaaagtgtg tgcaaggctg caggcactgg cagtgggaag aggcagacga ctagatgact 3420
tctgcacttt tagctgggtg aaaagtacca ctcccactct gaacatctgg ccgtccctgc 3480
aaagagtgtg ctgtgcttga agcagagcac tcacacataa atggctgtgt gtggaattgc 3540
ttgccaaaga agtttctagc ctttcccttt cccctaactg catcaggga gaattcttat 3600
ctctagcttg gtttccacat gaggtttttc tgagaagggc ttgggacaag aagtctgtca 3660
tgttagttaa gcaggcaaga aatcctacta atccagtttt gtttgaaagt tgtttgcctg 3720
tatgattttt taaaagtcaa gtttaatttc aaaaaacctt tttttctga gattactttt 3780
ggggtaatat ttaaaatgag agacattttg taaccctgta aaatacatag ggaatataac 3840
attccagtgt atacaaagaa ggcaaattct ttaatcaaat aaagcgtatt ataaaatgag 3900
aaaaaaaaaa aaaaaa 3916

```

<210> 35

<211> 511

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 35

```

Met Val Leu Leu Ala Ala Val Cys Thr Lys Ala Gly Lys Ala Ile
1      5      10      15
Val Ser Arg Gln Phe Val Glu Met Thr Arg Thr Arg Ile Glu Gly Leu
20     25     30
Leu Ala Ala Phe Pro Lys Leu Met Asn Thr Gly Lys Gln His Thr Phe
35     40     45
Val Glu Thr Glu Ser Val Arg Tyr Val Tyr Gln Pro Met Glu Lys Leu
50     55     60
Tyr Met Val Leu Ile Thr Thr Lys Asn Ser Asn Ile Leu Glu Asp Leu
65     70     75     80
Glu Thr Leu Arg Leu Phe Ser Arg Val Ile Pro Glu Tyr Cys Arg Ala
85     90     95
Leu Glu Glu Asn Glu Ile Ser Glu His Cys Phe Asp Leu Ile Phe Ala
100    105    110
Phe Asp Glu Ile Val Ala Leu Gly Tyr Arg Glu Asn Val Asn Leu Ala
115    120    125
Gln Ile Arg Thr Phe Thr Glu Met Asp Ser His Glu Glu Lys Val Phe
130    135    140
Arg Ala Val Arg Glu Thr Gln Glu Arg Glu Ala Lys Ala Glu Met Arg
145    150    155    160
Arg Lys Ala Lys Glu Leu Gln Gln Ala Arg Arg Asp Ala Glu Arg Gln
165    170    175
Gly Lys Lys Ala Pro Gly Phe Gly Gly Phe Gly Ser Ser Ala Val Ser
180    185    190
Gly Gly Ser Thr Ala Ala Met Ile Thr Glu Thr Ile Ile Glu Thr Asp
195    200    205
Lys Pro Lys Val Ala Pro Ala Pro Ala Arg Pro Ser Gly Pro Ser Lys
210    215    220
Ala Leu Lys Leu Gly Ala Lys Gly Lys Glu Val Asp Asn Phe Val Asp
225    230    235    240
Lys Leu Lys Ser Glu Gly Glu Thr Ile Met Ser Ser Ser Met Gly Lys
245    250    255
Arg Thr Ser Glu Ala Thr Lys Met His Ala Pro Pro Ile Asn Met Glu
260    265    270

```


Ser	Val	His	Met	Lys	Ile	Glu	Glu	Lys	Ile	Thr	Leu	Thr	Cys	Gly	Arg
		275					280					285			
Asp	Gly	Gly	Leu	Gln	Asn	Met	Glu	Leu	His	Gly	Met	Ile	Met	Leu	Arg
		290				295					300				
Ile	Ser	Asp	Asp	Lys	Tyr	Gly	Arg	Ile	Arg	Leu	His	Val	Glu	Asn	Glu
305					310					315					320
Asp	Lys	Lys	Gly	Val	Gln	Leu	Gln	Thr	His	Pro	Asn	Val	Asp	Lys	Lys
				325					330					335	
Leu	Phe	Thr	Ala	Glu	Ser	Leu	Ile	Gly	Leu	Lys	Asn	Pro	Glu	Lys	Ser
			340					345					350		
Phe	Pro	Val	Asn	Ser	Asp	Val	Gly	Val	Leu	Lys	Trp	Arg	Leu	Gln	Thr
		355					360					365			
Thr	Glu	Glu	Ser	Phe	Ile	Pro	Leu	Thr	Ile	Asn	Cys	Trp	Pro	Ser	Glu
		370				375					380				
Ser	Gly	Asn	Gly	Cys	Asp	Val	Asn	Ile	Glu	Tyr	Glu	Leu	Gln	Glu	Asp
385					390					395					400
Asn	Leu	Glu	Leu	Asn	Asp	Val	Val	Ile	Thr	Ile	Pro	Leu	Pro	Ser	Gly
				405					410					415	
Val	Gly	Ala	Pro	Val	Ile	Gly	Glu	Ile	Asp	Gly	Glu	Tyr	Arg	His	Asp
			420					425					430		
Ser	Arg	Arg	Asn	Thr	Leu	Glu	Trp	Cys	Leu	Pro	Val	Ile	Asp	Ala	Lys
			435				440					445			
Asn	Lys	Ser	Gly	Ser	Leu	Glu	Phe	Ser	Ile	Ala	Gly	Gln	Pro	Asn	Asp
						455					460				
Phe	Phe	Pro	Val	Gln	Val	Ser	Phe	Val	Ser	Lys	Lys	Asn	Tyr	Cys	Asn
465					470					475					480
Ile	Gln	Val	Thr	Lys	Val	Thr	Gln	Val	Asp	Gly	Asn	Ser	Pro	Val	Arg
				485					490					495	
Phe	Ser	Thr	Glu	Thr	Thr	Phe	Leu	Val	Asp	Lys	Tyr	Glu	Ile	Leu	
			500					505					510		